

Supplementary Appendix

This appendix has been provided by the authors to give readers additional information about their work.

Supplement to: Shirley MD, Tang H, Gallione CJ, et al. Sturge–Weber syndrome and port-wine stains caused by somatic mutation in *GNAQ*. *N Engl J Med* 2013;368:1971-9. DOI: 10.1056/NEJMoa1213507

Table of Contents

Methods	2
Figure S1. Venn diagram of 658 low confidence variants detected in affected tissue compared to normal tissue.	4
Figure S2. Multiple sequence alignment of 24 human guanine nucleotide-binding protein alpha subunits from heterotrimeric G proteins.....	5
Figure S3. Simulation of variant detection and resulting detection probabilities at varying read depth.....	9
Figure S4. MA plots of mutant allele frequencies in affected vs. normal tissues from subjects 1-3.	10
Table S1. Supplementary information about tissue samples from subjects in this study.	11
Table S2. Amplicon sequencing primer components.....	14
Table S3. Amplicon sequencing primers with barcodes.	15
Table S4. Targeted mutagenesis primer sequences.	18
Table S5. SNaPshot primer sequences.....	19
Table S6. Somatic variants detected in paired affected whole genome sequence.	20
Table S7. Allele frequencies from 1000 Genomes Project exomes.	49
File S1. Barcode file for de-multiplexing reads	60
File S2. Bpipe⁶ stage definitions and pipeline for aligning and de-multiplexing paired-end Illumina reads.	62
File S3. Shell script for splitting BWA aligned SAM files by barcode.....	63
File S4. Bpipe stage definitions and pipeline for counting alleles from de-multiplexed SAM files.....	64
File S5. Shell script for counting number of alleles from each mapped and de-multiplexed SAM file.....	65
References	66

Methods

Whole genome sequencing. Genomic DNA was purified from affected or unaffected tissue or blood from three individuals (n=6 samples) using a QIAGEN Puregene (blood samples) or DNAeasy (skin and brain) extraction kit and quantitated using a SYBR Green assay. Whole genome sequencing was performed on an Illumina HiSeq 2000 at Illumina, Inc. (San Diego, CA) to 33.3X to 50.8X mean depth of coverage. Paired-end reads were aligned to the hg19 human reference using the Illumina Genome Analyzer Pipeline. Somatic single nucleotide variants (SNVs) or insertion / deletions (indels) were detected using Strelka.¹ Post-call filtration was applied using the program author's recommended parameters to remove spurious SNVs and indels resulting from homo-polymer repeats and abnormally high read depth regions. Somatic SNV calls from Strelka (from autosomes as well as X chromosome) to the affected samples were identified, and mutant allele frequencies were calculated for each affected/normal pair of WGS. These were identified as potential somatic SNVs. These SNV calls were annotated and ranked in order of predicted functional effect using VAAST.² 1000 Genomes variants were specified as background to remove variants found in a normal population, and RefSeq genes were used as regions of interest.

Targeted amplicon sequencing. An amplicon consisting of 168 bp from *GNAQ* exon 4 and adjacent intronic sequence (NC_000009.11 80,412,463-80,412,630), encompassing the *GNAQ* c.548G residue (NM_002072.3), was PCR amplified in a two-stage reaction. For each sample a unique DNA barcode, sequencing adapters, and Illumina flow-cell clustering adapters were added (**Tables S2 and S3**). Barcode sequences (**File S1**) were generated using a 7 nucleotide Hamming encoding scheme³ allowing for correction of a single base miscall. Paired-end sequencing of barcoded amplicons was performed using an Illumina MiSeq, producing 151 nt paired-end reads. Reads were aligned to the hg19 human reference using BWA 0.6.2⁴ with base quality trimming Q30. SAMtools⁵ mpileup of base calls greater than Q30 was used to determine allele counts at the mutation site. Bpipe⁶ pipelines and Bash scripts are provided (**Files S2-S5**). Aligned exome reads from the 1000 Genomes Project{Consortium:2011gj} (alignment release 2011-11-14) were evaluated at the c.548 position for base calls supporting the c.548G>A mutation. Only exomes having a read depth of greater than 100 at the variant site were evaluated. Samples from both amplicon sequencing and 1000 Genomes Project exomes were determined to have a mutation if the percent of reads supporting a mutation exceeded 10 times (1%) the expected base miscall rate (0.1%). The median read depth for amplicon sequencing was selected on the basis of 1,000,000 simulations of a random draw from an allele pool with 1% mutant allele frequency (**Figure S3**).

Plasmids. Full length wild-type GNAQ plasmid was purchased from Origene (Rockville, MD). This TruORF Gold clone contains the entire reading frame plus Myc and flag epitope tags at the carboxyl terminus. Specific mutations, c.548G>A, p.Arg183Gln, and c.626A>T, p.Gln209Leu, were introduced into the clone using primers for site directed mutagenesis (**Table S4**). Clones were sequenced to verify that no other changes were present. pSRE(serum response element)-Luc (Agilent Technologies) and pSV40-RL (Roche) were used as reporter plasmids for the luciferase assay.

Cell culture and Western blotting. Human embryonic kidney HEK293T (293T) cells (ATCC, Manassas, VA) were maintained in Dulbecco's Modified Eagle's Medium (DMEM, Gibco) containing 10% fetal bovine serum at 37°C in 5% CO₂. Cells were grown on 100 mm² plates and transfected with 6μg plasmid DNA using FuGENE 6 (Promega) according to the manufacturer's protocol. Cell lysates were analyzed by western blotting using standard methods. Antibodies recognizing p44/42 MAPK (Erk1/2) (#9102), Phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204, #9101), p38 MAPK (#9212), Phospho-p38 MAPK (Thr180/Tyr182, #9211), Akt (#9272) Phospho-Akt (Ser473, #4058), MARCKS (#5607), Phospho-MARCKS (Ser167/170 #8722) and Phospho-JNK (Thr183/Tyr185 #9251) were obtained from Cell Signaling Technology. JNK (SC-474) antibodies were obtained from Santa Cruz. Mouse anti-Flag M2 (1:1000, Sigma) and mouse anti-alpha tubulin (1:500, DSHB, U. of Iowa) were also used. Protein bands were visualized using secondary antibodies conjugated to HRP (1:3000, BioRad) followed by incubation with Pierce SuperSignal West Pico Chemiluminescent Substrate (Thermo Fisher Scientific, Rockford, IL) and analyzed using the G:BOX gel documentation system (Syngene). Tetradecanoylphorbol acetate (TPA #4174) was obtained from Cell Signaling Technology, and used at 200nM for 20-30 mins.

Luciferase Assay. GNAQ, GNAQ p.Arg183Gln, or GNAQ p.Gln209Leu, pSRE-Luc and pSV40-RL, at a ratio of 5:200:1 ng, were transfected into 293T cells using FuGENE 6 (Promega). Cells were lysed after 20 – 24 hours incubation and the luciferase activity was measured using the Dual-Luciferase Reporter Assay System (Promega) on a Polarstar Optima plate reader (BMG Labtech, Germany).

SNaPshot Assay. DNA was extracted from archived, formalin-fixed, paraffin-embedded PWS samples according to the manufacturer's protocol (Gentra Puregene, QIAGEN). Primers for exon 4 of *GNAQ* (**Table S5**) were used to amplify genomic DNA from each of the samples and electrophoresed on a 1% agarose gel. PCR products were extracted using GeneClean Turbo (MP Bio). Purified PCR products were interrogated for their sequence at position c.548 using the SNaPshot Multiplex Kit (Life Technologies, Grand Island, NY) and analyzed on an ABI Prism 3130. Reference and mutant allele frequencies were calculated based on the area of the resulting peaks.

Author Roles. JP, DM, and AC designed the paired whole genome sequencing study. LF processed DNA for whole genome and amplicon sequencing. MS designed, analyzed and vouched for the amplicon sequencing study. MS and JB analyzed data from whole genome sequencing, and MS vouched for the analysis. CG designed, gathered, analyzed, and vouched for data from luciferase assays. HT designed, gathered, analyzed, and vouched for data from Western blots. CG designed, gathered, analyzed, and vouched for data from SNaPshot assays. AC provided patient and MRI images. MS, HT, CG, JB, PN, AC, DM, and JP provided comments and editing of the manuscript. MS and JP authored the manuscript.

Figure S1. Venn diagram of 658 low confidence variants detected in affected tissue compared to normal tissue.

Numbers in parentheses are protein coding non-synonymous variants. Of the 10 variants shared by all three subjects, the single non-synonymous variant corresponded to *GNAQ*.

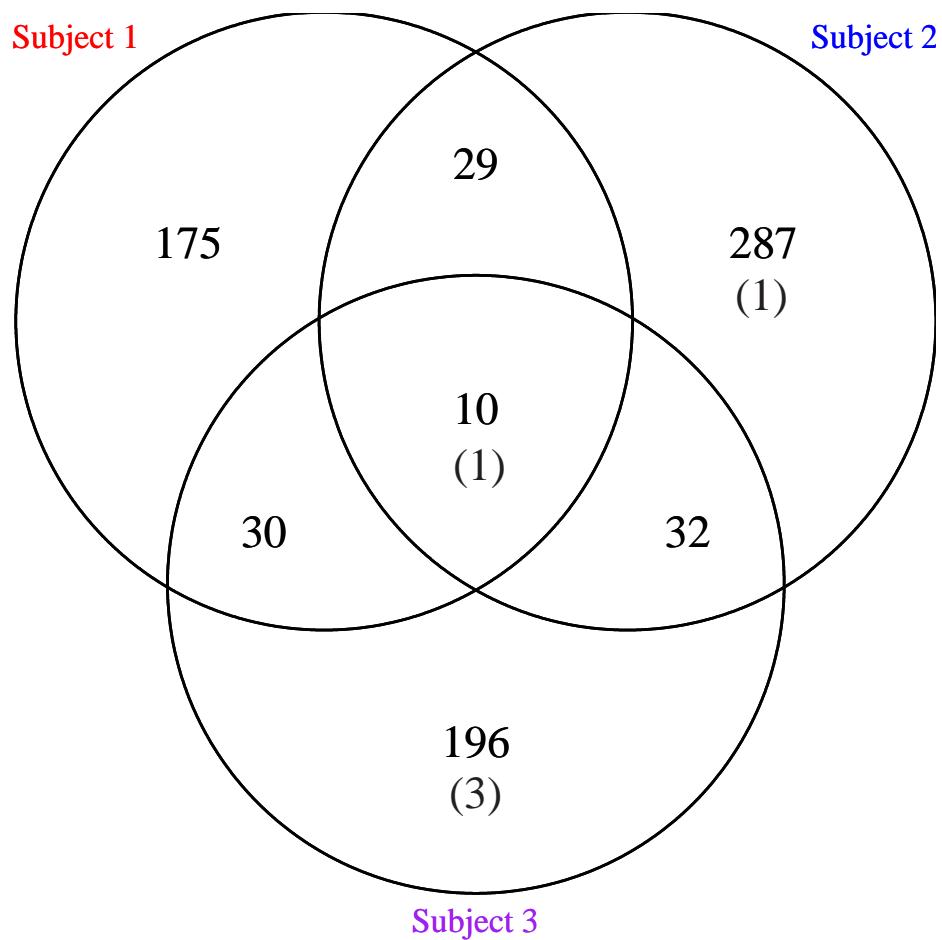


Figure S2. Multiple sequence alignment of 24 human guanine nucleotide-binding protein alpha subunits from heterotrimeric G proteins.

For protein ALEX XLas (NP_536350.2) which has an extended amino terminus the first 457 residues are truncated. The alignment was generated using ClustalW2 with default settings. Bold font indicates the aligned residue at which the Arg183Gln mutation occurred in GNAQ. The accession numbers are as follows: G(q)_alpha (NP_002063.2), G_alpha-11 (NP_002058.2), G_alpha-12 (NP_031379.2), G_alpha-13 (NP_006563.2), G_alpha-14 (NP_004288.1), G_alpha-15 (NP_002059.2), GNASS (NP_536351.1), GNASL (NP_000507.1), G(s) (protein ALEX isoform-f; NP_001070956.1), G(s) (protein_ALEX_XLas; NP_536350.2), G(s) (protein_ALEX_isoform-g; NP_001070957.1), G(t)_alpha-1 (NP_000163.2), G(t)_alpha-2 (NP_005263.1), G(t)_alpha-3 (NP_001095856.1), G(i)_alpha-1_isoform-1 (NP_002060.4), G(i)_alpha-1_isoform-2 (NP_001243343.1), G(i)_alpha-2_isoform-1 (NP_002061.1), G(i)_alpha-2_isoform-2 (NP_001159897.1), G(o)_alpha_isoform-a (NP_066268.1), G(o)_alpha_isoform-b (NP_620073.2), G(k)_alpha (NP_006487.1), G(z)_alpha (NP_002064.1), G(olf)_alpha_isoform-1 (NP_892023.1), G(olf)_alpha_isoform-2 (NP_001135811.1).

G_q_alpha	-----	
G_alpha-11	-----	
G_alpha-12	-----	
G_alpha-13	-----	
G_alpha-14	-----	
G_alpha-15	-----	
G_s_protein_ALEX_GNASS	-----	
G_s_protein_ALEX_GNASL	-----	
G_s_protein_ALEX_isoform-f	-----	
G_s_protein_ALEX_XLas	-----	ASAWRGKSESSRGRRVYYDEGVASSDDSSGDESDDGTSGCLRWFQHRRN 50
G_s_protein_ALEX_isoform-g	-----	
G_t_alpha-1	-----	
G_t_alpha-2	-----	
G_t_alpha-3	-----	
G_i_alpha-1_isoform-1	-----	
G_i_alpha-1_isoform-2	-----	
G_i_alpha-2_isoform-1	-----	
G_i_alpha-2_isoform-2	-----	
G_o_alpha_isoform-a	-----	
G_o_alpha_isoform-b	-----	
G_k_alpha	-----	
G_z_alpha	-----	
G_olf_alpha_isoform-1	-----	MGLCYSLRPLLFGGPDDPCAASEPPVEDAQPAPALAPVRAAARDTAR 50
G_olf_alpha_isoform-2	-----	MG-----CLGG-----6
 G_q_alpha	-----	
G_alpha-11	-----	-----MTLESIMACC-----10
G_alpha-12	-----	-----MTLESMMACC-----10
G_alpha-13	-----	-----MSGVVRTLCSRCLLPAAEAGGARERR-----24
G_alpha-14	-----	-----MADFLP--SRSVLSVCFPGCLLT-----21
G_alpha-15	-----	-----MAGCCC-----6
G_s_protein_ALEX_GNASS	-----	-----MARSILTWRCCP-----11
G_s_protein_ALEX_GNASL	-----	-----MGCLGNNSKTE-----10
G_s_protein_ALEX_isoform-f	-----	-----MGCLGNNSKTE-----10
G_s_protein_ALEX_XLas	-----	-----MGCLGNNSKTE-----10
G_s_protein_ALEX_isoform-g	-----	-----RRRRKPQRNLLRNFLVQAFGGCFGRSESPQPKASRSLKVKKVPLAEKRRQ 100
G_t_alpha-1	-----	-----MGCLGNNSKTE-----10
G_t_alpha-2	-----	-----MGAG-----4
G_t_alpha-3	-----	-----MGSG-----4
G_i_alpha-1_isoform-1	-----	-----MGSG-----4
G_i_alpha-1_isoform-2	-----	-----MGCT-----4
G_i_alpha-2_isoform-1	-----	-----MGCT-----4
G_i_alpha-2_isoform-2	-----	-----MGCT-----4
G_o_alpha_isoform-a	-----	-----MGCT-----4
G_o_alpha_isoform-b	-----	-----MGCT-----4
G_k_alpha	-----	-----MGCR-----4
G_z_alpha	-----	-----TLLPRGGEGSPACARPkadkpkekrqrte-----79
G_olf_alpha_isoform-1	-----	-----NSKTTE-----12
G_olf_alpha_isoform-2	-----	 -----LSEE-----AKEARRINDEIERQLRRDKRDARRELKLL 43
 G_q_alpha	-----	-----LSDE-----VKESKRINAIEIEKQLRRDKRDARRELKLL 43
G_alpha-11	-----	-----AGSGARD-----EREARRRSRDIALLARERRAVRRLVKIL 61
G_alpha-12	-----	-----SG-----EAEQQRKSKEIDKCLSREKTYVKRLVKIL 52
G_alpha-13	-----	-----LSAE-----EKESQRISAEIERQLRRDKDARRELKLL 39
G_alpha-14	-----	

G_alpha-14	SVILFLNKKDLLEEKIM--YSHLISYFPEYTGPQDVRAAR-----	302
G_alpha-15	SVILFLNKTIDILEEKIP--TSHLATYFPSFQGPQDAEAAK-----	309
G_s_protein_ALEX_GNASS	SVILFLNKQDLLAEKVLAGKS KIEDYFPEFARYTTPEDATPEPGEDPRVT	321
G_s_protein_ALEX_GNASL	SVILFLNKQDLLAEKVLAGKS KIEDYFPEFARYTTPEDATPEPGEDPRVT	335
G_s_protein_ALEX_isoform-f	SVILFLNKQDLLAEKVLAGKS KIEDYFPEFARYTTPEDATPEPGEDPRVT	336
G_s_protein_ALEX_XLas	SVILFLNKQDLLAEKVLAGKS KIEDYFPEFARYTTPEDATPEPGEDPRVT	431
G_s_protein_ALEX_isoform-g	SVILFLNKQDLLAEKVLAGKS KIEDYFPEFARYTTPEDATPEPGEDPRVT	320
G_t_alpha-1	SIVLFLNKKDVFEEKIK--KAHLSICFPDYDGPNTYEDAGN-----	297
G_t_alpha-2	SIVLFLNKKDLFEEKIK--KVHLSICFPDYDGPNTYEDAGN-----	301
G_t_alpha-3	SIVLFLNKKDIFQEKVT--KVHLSICFPDYDGPNTYEDAGN-----	301
G_i_alpha-1_isoform-1	SIILFLNKKDLFEEKIK--KSPLTICYPEYAGSNTYEEAAA-----	301
G_i_alpha-1_isoform-2	SIILFLNKKDLFEEKIK--KSPLTICYPEYAGSNTYEEAAA-----	249
G_i_alpha-2_isoform-1	SIILFLNKKDLFEEKIT--HSPLTICFPEYTGAN KYDEAAS-----	302
G_i_alpha-2_isoform-2	SIILFLNKKDLFEEKIT--HSPLTICFPEYTGAN KYDEAAS-----	265
G_o_alpha_isoform-a	SIILFLNKKDLFGEKIK--KSPLTICFPEYTGPNTYEDAAA-----	302
G_o_alpha_isoform-b	SIILFLNKKDIFEKEKIK--KSPLTICFPEYTGPSAFTEAVA-----	302
G_k_alpha	SIILFLNKKDIFEKEKIK--RSPLTICYPEYTSNTYEEAAA-----	301
G_z_alpha	SLILFLNKKDLLAEKIR--RIPLTICFPEYKGQNTYEEAV-----	302
G_olf_alpha_isoform-1	SIILFLNKQDMLAEKVLAGKS KIEDYFPEYANYTVPEDATPDAGEDPKVT	399
G_olf_alpha_isoform-2	SIILFLNKQDMLAEKVLAGKS KIEDYFPEYANYTVPEDATPDAGEDPKVT	322
*:***** * : * : : . :		
G_q_alpha	--EFILKMFVDL----NPDSDK----IIYSHFTCATDTENIRFVF	341
G_alpha-11	--EFILKMFVDL----NPDSDK----IIYSHFTCATDTENIRFVF	341
G_alpha-12	--RYLVQCFCDRK----RRNRNS----KPLFHHTTAIDTENVRFVF	363
G_alpha-13	--KFLVECFRNK----RRDQQQ----KPLYHHFTTAINTENIRLVF	359
G_alpha-14	--DFILKLYQDQ----NPDEKE----VIYSHFTCATDTDNIRFVF	337
G_alpha-15	--RFILEDMYTRMYTGCVDPEGSKKGARSRLFSHYTCATDTQNIRKVF	356
G_s_protein_ALEX_GNASS	RAKYFIRDEFRLRISTASGDGRHYCY-----PHFTCAVDTENIRVF	362
G_s_protein_ALEX_GNASL	RAKYFIRDEFRLRISTASGDGRHYCY-----PHFTCAVDTENIRVF	376
G_s_protein_ALEX_isoform-f	RAKYFIRDEFRLRISTASGDGRHYCY-----PHFTCAVDTENIRVF	377
G_s_protein_ALEX_XLas	RAKYFIRDEFRLRISTASGDGRHYCY-----PHFTCAVDTENIRVF	472
G_s_protein_ALEX_isoform-g	RAKYFIRDEFRLRISTASGDGRHYCY-----PHFTCAVDTENIRVF	361
G_t_alpha-1	-----YIKVQFLELMNMRDVKEIYS-----HMTCATDTQNVKFVF	332
G_t_alpha-2	-----YIKSQFLDLNMRKDVKIEIYS-----HMTCATDTQNVKFVF	336
G_t_alpha-3	-----YIKNQFLDLNLKKEDKEIYS-----HMTCATDTQNVKFVF	336
G_i_alpha-1_isoform-1	-----YIQCQFEDLNKRKDTEIYT-----HFTCATDTKNVQFVF	336
G_i_alpha-1_isoform-2	-----YIQCQFEDLNKRKDTEIYT-----HFTCATDTKNVQFVF	284
G_i_alpha-2_isoform-1	-----YIQSKFEDLNKRKDTEIYT-----HFTCATDTKNVQFVF	337
G_i_alpha-2_isoform-2	-----YIQSKFEDLNKRKDTEIYT-----HFTCATDTKNVQFVF	300
G_o_alpha_isoform-a	-----YIQAQFESKNR-SPNKEIYC-----HMTCATDTNNI QVVF	336
G_o_alpha_isoform-b	-----YIQAQYESKNK-SAHKEIYT-----HVCATDTNNI QFVF	336
G_k_alpha	-----YIQCQFEDLNRRKDTEIYT-----HFTCATDTKNVQFVF	336
G_z_alpha	-----YIQRQFEDLNRRKETKEIYS-----HFTCATDTSNI QFVF	337
G_olf_alpha_isoform-1	RAKFFIRDLFLRISTATGDGKHYCY-----PHFTCAVDTENIRVF	440
G_olf_alpha_isoform-2	RAKFFIRDLFLRISTATGDGKHYCY-----PHFTCAVDTENIRVF	363
*: * * :*. * : * *		
G_q_alpha	AAVKDTILQLNLKEYNLV	359
G_alpha-11	AAVKDTILQLNLKEYNLV	359
G_alpha-12	HAVKDTILQENLKDMIQ	381
G_alpha-13	RDVKDTILHDNLKQLMLQ	377
G_alpha-14	AAVKDTILQLNLREFNLV	355
G_alpha-15	KDVRDSVLARYLDEINLL	374
G_s_protein_ALEX_GNASS	NDCRDIIQRMHLRQYELL	380
G_s_protein_ALEX_GNASL	NDCRDIIQRMHLRQYELL	394
G_s_protein_ALEX_isoform-f	NDCRDIIQRMHLRQYELL	395
G_s_protein_ALEX_XLas	NDCRDIIQRMHLRQYELL	490
G_s_protein_ALEX_isoform-g	NDCRDIIQRMHLRQYELL	379
G_t_alpha-1	DAVTDDIIKENLKDCCGLF	350
G_t_alpha-2	DAVTDDIIKENLKDCCGLF	354
G_t_alpha-3	DAVTDDIIKENLKDCCGLF	354
G_i_alpha-1_isoform-1	DAVTDVIICKNNLKDCGLF	354
G_i_alpha-1_isoform-2	DAVTDVIICKNNLKDCGLF	302
G_i_alpha-2_isoform-1	DAVTDVIICKNNLKDCGLF	355
G_i_alpha-2_isoform-2	DAVTDVIICKNNLKDCGLF	318
G_o_alpha_isoform-a	DAVTDIIIANNLRCGGLY	354
G_o_alpha_isoform-b	DAVTDVIIAKNLRCGGLY	354
G_k_alpha	DAVTDVIICKNNLKDCGLF	354
G_z_alpha	DAVTDVIICKNNLKDCGLF	355
G_olf_alpha_isoform-1	NDCRDIIQRMHLKQYELL	458
G_olf_alpha_isoform-2	NDCRDIIQRMHLKQYELL	381
*: * *		

Figure S3. Simulation of variant detection and resulting detection probabilities at varying read depth.

Simulation was performed using 1,000,000 draws from an allele pool with 1% mutant allele frequency at read depths from 1 to 10,192 using a detection threshold for genotype determination of 0.5% mutant allele.

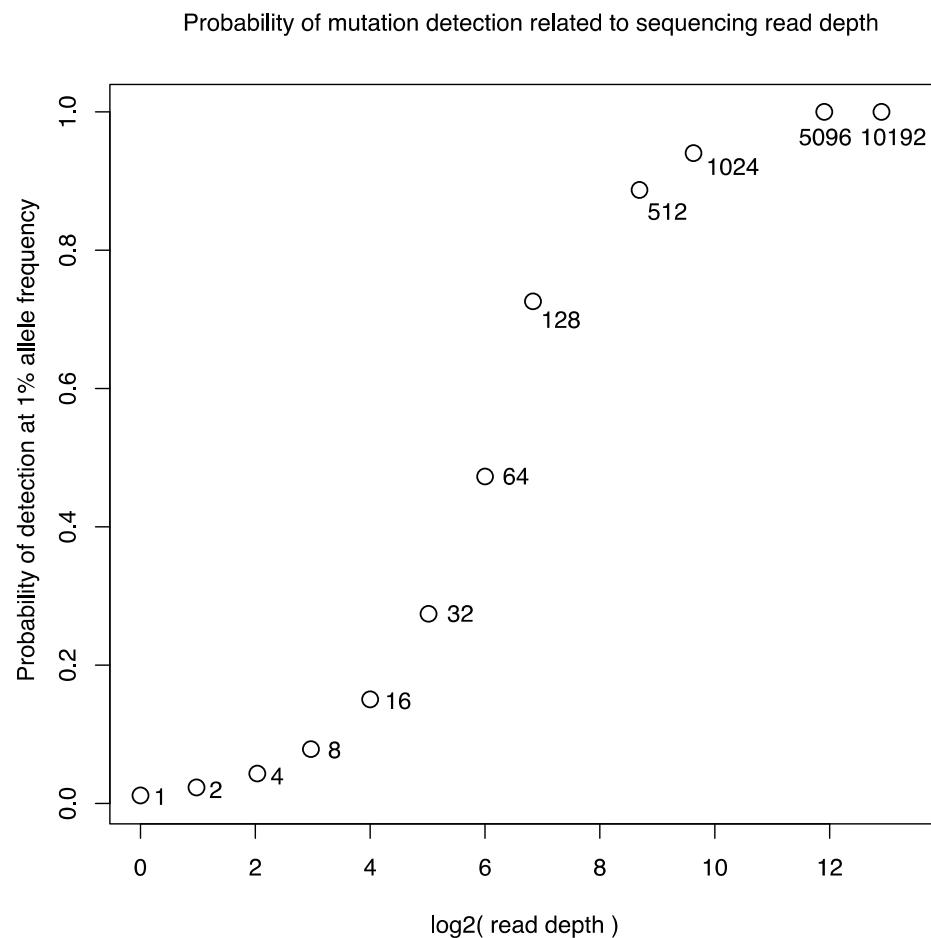


Figure S4. MA plots of mutant allele frequencies in affected vs. normal tissues from subjects 1-3.

Each data point corresponds to a variant called by Strelka. Left panels: Red data points represent private variants (unique to the indicated subject). Black data points represent variant sites identified by Strelka in other subjects. Center panels: private variants (unique to the indicated subject). Right panels: variant sites identified by Strelka in other subjects. M represents the sum of log transformed allele frequencies (affected/unaffected), with positive values corresponding to higher frequencies. A represents the difference of log transformed allele frequencies (affected/unaffected), with positive values corresponding to greater differences between the frequencies in affected and unaffected samples. In each panel there is a major cluster of data points (blue ellipse) corresponding to relatively high frequency variants that have little difference between affected and unaffected samples. A second cluster (green ellipse) represents variants that occur at elevated frequency in the affected sample, and near zero frequency in the unaffected sample.

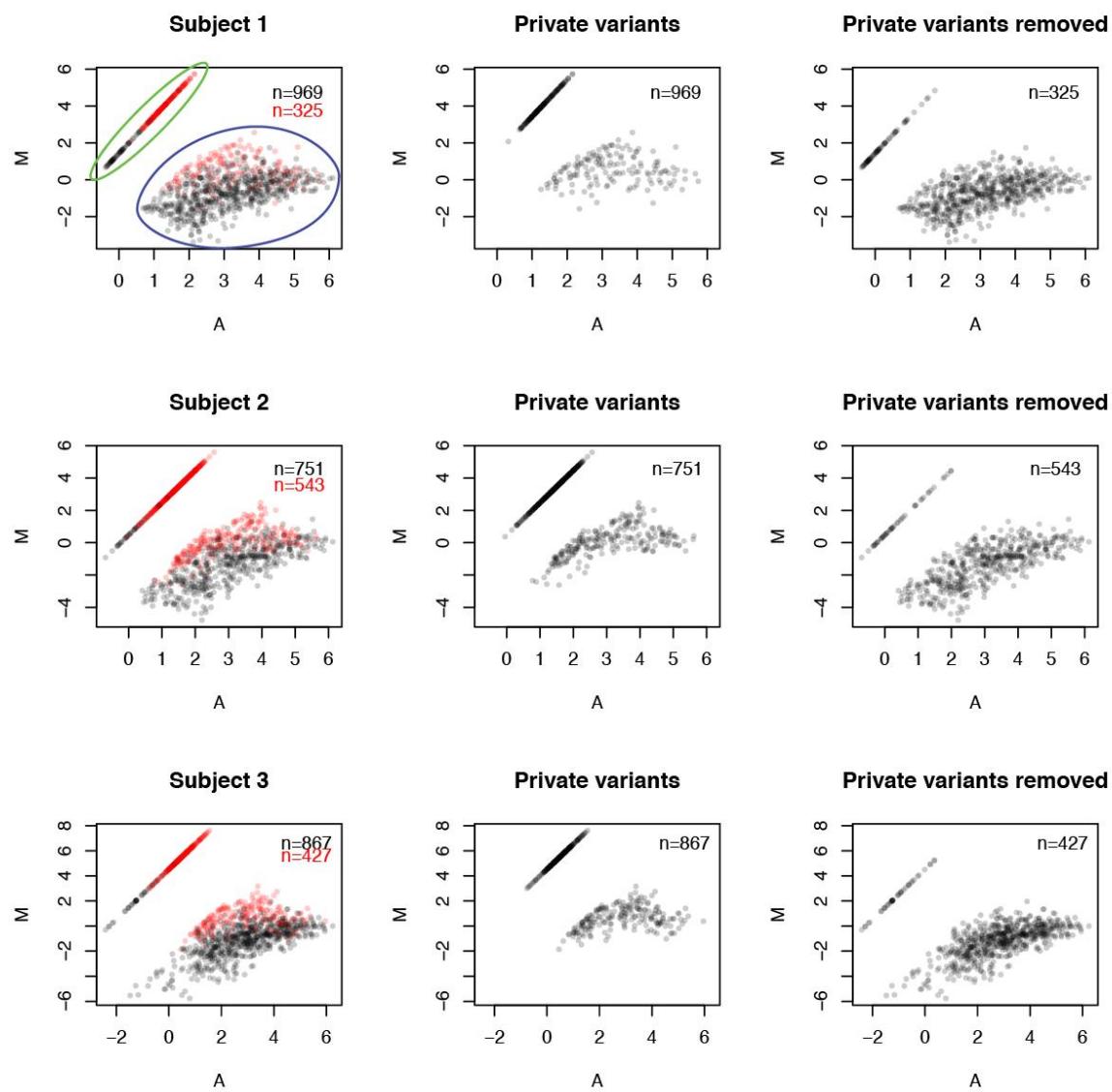


Table S1. Supplementary information about tissue samples from subjects in this study.

Columns: (Sample) Continuous numbering system providing an indexing system for Table 1 and Table 2. (ID) Numbering system grouping all samples corresponding to the same subject. (Diagnosis) Clinical diagnosis as indicated in patient medical records. (PWS) Indication of whether skin sample was from a PWS or visibly normal skin. (Tissue) Tissue that sample was obtained from. (Replicate) Indication of whether results from replicate samples from the same individual were technical or biological in nature. (R183Q) Indication of the presence of p.Arg183Gln amino acid substitution in each sample. (% Mutant Allele) Percentage of mutant allele c.548G>A in each sample, either determined by chromatogram peak height or $A \text{ counts} \div (G \text{ counts} + A \text{ counts}) * 100$. (G counts) Number of reads supporting a G allele at a base quality score greater than 30. (A counts) Number of reads supporting an A allele at a base quality score greater than 30. (Read Depth) Number of reads supporting G or A alleles at base quality score greater than 30. (Method) Technique used to determine presence of c.548G>A – see methods section of manuscript. (Accession) NICHD Brain and Tissue Bank accession number. (Sex) Biological gender of sample. (Age) Age of sample in years (y), days (d) and months (m). (Ethnicity) Reported ethnicity of subjects. (Clinical Info) Clinically relevant information pertaining to source and description of tissue sample and subject.

Sample	ID	Diagnosis	PWS	Tissue	Replicate	R183Q	%Mutant Allele	G counts	A counts	Read Depth	Method	Accession	Sex	Age	Ethnicity	Clinical Info
1	1	SWS	Yes	skin	-	Yes	3.6	11728	438	12166	Amplicon Seq	UMB1148	F	1yr65d	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
2	1	SWS	No	skin	-	No	0.1	8234	9	8243	Amplicon Seq	UMB1148	F	1yr65d	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
3	2	SWS	Yes	skin	-	Yes	3.2	13796	452	14248	Amplicon Seq	UMB1176	F	4y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
4	2	SWS	No	skin	-	No	0.1	11074	14	11088	Amplicon Seq	UMB1176	F	4y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
5	3	SWS	Yes	skin	Technical	Yes	6.1	12923	834	13757	Amplicon Seq	UMB1180	F	-	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
6	3	SWS	Yes	skin	Technical	Yes	6.5	55845	3854	59699	Amplicon Seq	UMB1180	F	-	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
7	3	SWS	No	skin	Technical	No	0.6	9420	59	9479	Amplicon Seq	UMB1180	F	-	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
8	3	SWS	No	skin	Technical	No	0.9	40161	375	40536	Amplicon Seq	UMB1180	F	-	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
9	4	SWS	Yes	skin	Technical	Yes	4.5	9861	466	10327	Amplicon Seq	UMB1197	F	7.5y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
10	4	SWS	Yes	skin	Technical	Yes	3.5	39980	1448	41428	Amplicon Seq	UMB1197	F	7.5y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
11	4	SWS	No	skin	Technical	No	0.1	11339	15	11354	Amplicon Seq	UMB1197	F	7.5y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
12	4	SWS	No	skin	Technical	No	0.9	2424	22	2446	Amplicon Seq	UMB1197	F	7.5y	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
13	5	SWS	Yes	skin	-	Yes	3.4	12202	427	12629	Amplicon Seq	UMB1263	F	132d	Caucasian	Skin biopsy NICHD Brain and Tissue Bank
14	5	SWS	No	skin	-	No	0.1	11500	13	11513	Amplicon Seq	UMB1263	F	132d	Caucasian	Skin biopsy NICHD Brain and Tissue Bank
15	6	SWS	Yes	skin	-	Yes	4.0	16769	697	17466	Amplicon Seq	UMB1382	F	14y320d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
16	7	SWS	Yes	skin	Technical	Yes	2.2	13860	306	14166	Amplicon Seq	UMB1424	F	37y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
17	7	SWS	No	skin	Technical	No	0.1	10358	9	10367	Amplicon Seq	UMB1425	F	38y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
18	7	SWS	Yes	skin	Technical	Yes	2.1	54703	1147	55850	Amplicon Seq	UMB1426	F	37y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
19	7	SWS	No	skin	Technical	Yes	2.0	91151	1857	93008	Amplicon Seq	UMB1427	F	38y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
20	8	SWS	Yes	skin	-	Yes	4.1	9401	400	9801	Amplicon Seq	UMB1692	F	3y70d	Caucasian	Skin biopsy, NICHD Brain and Tissue Bank
21	8	SWS	No	skin	-	No	0.1	16099	10	16109	Amplicon Seq	UMB1692	F	3y70d	Caucasian	Skin biopsy NICHD Brain and Tissue Bank
22	9	PWS only	Yes	skin	-	Yes	5.6	39377	2326	41703	Amplicon Seq		M	63 y	Caucasian	Skin biopsy from PWS on leg
23	10	PWS only	Yes	skin	-	Yes	2.8	57585	1634	59219	Amplicon Seq		F	45 Y	Caucasian	Skin biopsy from PWS on left shoulder

24	10	PWS only	No	skin	-	Yes	1.1	12799	148	12947	Amplicon Seq		F	45 Y	Caucasian	Skin biopsy from right shoulder
25	11	PWS only	Yes	skin	-	Yes	6.7	-	-	-	SNaPshot		F	-	-	-
26	12	PWS only	Yes	skin	-	No	0.0	-	-	-	SNaPshot		M	74y7m	Caucasian	V1V2 left face
27	13	PWS only	Yes	skin	-	Yes	5.9	-	-	-	SNaPshot		M	20y	Caucasian	V1V2 with lip hypertrophy
28	14	PWS only	Yes	skin	-	Yes	6.2	-	-	-	SNaPshot		M	27y	Asian	V1V2 with lip hypertrophy
29	15	PWS only	Yes	skin	-	Yes	14.2	-	-	-	SNaPshot		F	40y	Caucasian	Cheek and lip
30	16	PWS only	Yes	skin	-	Yes	1.7	-	-	-	SNaPshot		-	-	-	-
31	17	PWS only	Yes	skin	-	Yes	4.5	-	-	-	SNaPshot		F	29y2m	Asian	Lip hypertrophy
32	18	PWS only	Yes	skin	-	Yes	5.3	-	-	-	SNaPshot		M	64y7m	Caucasian	Lip hypertrophy
33	19	PWS only	Yes	skin	-	Yes	4.7	-	-	-	SNaPshot		M	-	Caucasian	Lip hypertrophy
34	20	PWS only	Yes	skin	-	Yes	4.3	-	-	-	SNaPshot		M	13y11m	Caucasian	Lip hypertrophy
35	21	PWS only	Yes	skin	-	Yes	18.1	-	-	-	SNaPshot		F	54y11m	Caucasian	Lip hypertrophy
36	22	SWS	Yes	skin	-	Yes	5.0	-	-	-	SNaPshot		F	31y8m	Caucasian	Lip hypertrophy
37	7	SWS	-	brain	Biol.	Yes	5.6	9981	589	10570	Amplicon Seq	UMB1428	F	39y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
38	7	SWS	-	brain	Biol.	Yes	5.6	12198	728	12926	Amplicon Seq	UMB1429	F	36y	Caucasian	Died of leukemia, autopsy, NICHD Brain and Tissue Bank
39	23	SWS	-	brain	Biol.	Yes	5.8	11360	697	12057	Amplicon Seq	UMB1130	F	1y12d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
40	23	SWS	-	brain	Biol.	Yes	5.6	17804	1049	18853	Amplicon Seq	UMB1130	F	1y12d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
41	24	SWS	-	brain	Biol.	Yes	3.5	15265	555	15820	Amplicon Seq	UMB1262	M	5y35d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
42	24	SWS	-	brain	Biol.	Yes	2.7	15510	425	15935	Amplicon Seq	UMB1262	M	5y35d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
43	25	SWS	-	brain	Biol.	No	0.1	17511	17	17528	Amplicon Seq	UMB1468	F	15y89d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
44	25	SWS	-	brain	Biol.	No	0.0	9817	2	9819	Amplicon Seq	UMB1468	F	15y89d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
45	26	SWS	-	brain	Biol.	No	0.1	12199	18	12217	Amplicon Seq	UMB1604	F	6y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
46	26	SWS	-	brain	Biol.	No	0.1	14425	19	14444	Amplicon Seq	UMB1604	F	6y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
47	26	SWS	-	brain	Biol.	Yes	3.1	11147	352	11499	Amplicon Seq	UMB1604	F	6y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
48	26	SWS	-	brain	Biol.	Yes	1.4	17763	256	18019	Amplicon Seq	UMB1604	F	6y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
49	27	SWS	-	brain	Biol.	Yes	5.1	14774	798	15572	Amplicon Seq	UMB1658	M	10mo	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
50	27	SWS	-	brain	Biol.	Yes	2.2	11887	266	12153	Amplicon Seq	UMB1658	M	10mo	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
51	28	SWS	-	brain	Biol.	Yes	7.3	12896	1010	13906	Amplicon Seq	UMB1699	F	2y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
52	28	SWS	-	brain	Biol.	Yes	8.1	9818	869	10687	Amplicon Seq	UMB1699	F	2y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
53	28	SWS	-	brain	Biol.	Yes	7.6	14473	1192	15665	Amplicon Seq	UMB1699	F	2y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
54	28	SWS	-	brain	Biol.	Yes	7.0	9473	708	10181	Amplicon Seq	UMB1699	F	2y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
55	29	SWS	-	brain	Biol.	Yes	9.9	10934	1205	12139	Amplicon Seq	UMB1729	M	3y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
56	29	SWS	-	brain	Biol.	Yes	7.4	11986	957	12943	Amplicon Seq	UMB1729	M	3y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
57	29	SWS	-	brain	Biol.	Yes	11.1	13754	1726	15480	Amplicon Seq	UMB1729	M	3y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
58	29	SWS	-	brain	Biol.	Yes	6.1	14133	924	15057	Amplicon Seq	UMB1729	M	3y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
59	29	SWS	-	brain	Biol.	Yes	6.0	13701	881	14582	Amplicon Seq	UMB1729	M	3y	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
60	30	SWS	-	brain	-	Yes	4.1	17651	762	18413	Amplicon Seq		F	11m	-	Surgical Tissue
61	31	SWS	-	brain	-	Yes	4.8	8068	405	8473	Amplicon Seq		F	11m	-	Surgical Tissue
62	32	SWS	-	brain	Biol.	No	0.7	3509	26	3535	Amplicon Seq		M	2.5y	-	Surgical Tissue
63	32	SWS	-	brain	Biol.	No	0.6	12560	73	12633	Amplicon Seq		M	2.5y	-	Surgical Tissue
64	32	SWS	-	brain	Biol.	No	0.2	11048	24	11072	Amplicon Seq		M	2.5y	-	Surgical Tissue
65	32	SWS	-	brain	Biol.	Yes	1.5	3585	54	3639	Amplicon Seq		M	2.5y	-	Surgical Tissue
66	33	SWS	-	brain	Biol.	Yes	5.7	10928	665	11593	Amplicon Seq	UMB4575	M	7y4m	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
67	33	SWS	-	brain	Biol.	Yes	4.0	17756	748	18504	Amplicon Seq	UMB4575	M	7y4m	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
68	34	SWS	-	brain	Biol.	No	0.1	14846	8	14854	Amplicon Seq	UMB4613	M	19y352d	Caucasian	Bilateral brain, died by car accident NICHD Brain and Tissue Bank

69	34	SWS	-	brain	Biol.	No	0.1	11372	14	11386	Amplicon Seq	UMB4613	M	19y352d	Caucasian	Bilateral brain, died by car accident NICHD Brain and Tissue Bank
70	35	SWS	-	brain	Biol.	No	0.2	47891	87	47978	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB
71	35	SWS	-	brain	Biol.	No	0.1	9657	12	9669	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB, died from complications of SWS
72	35	SWS	-	brain	Biol.	No	0.1	15271	10	15281	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB, died from complications of SWS
73	35	SWS	-	brain	Biol.	No	0.1	16717	15	16732	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB
74	35	SWS	-	brain	Biol.	No	0.0	14341	7	14348	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB
75	35	SWS	-	brain	Biol.	No	0.4	50906	184	51090	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB, died from complications of SWS
76	35	SWS	-	brain	Biol.	Yes	1.5	6000	92	6092	Amplicon Seq	UMB4660	F	5y12d	Caucasian	Diagnosis "bilateral" brain, postmortem at NICHD BTB
77	36	SWS	-	brain	Biol.	No	0.4	69105	290	69395	Amplicon Seq	UMB4731	M	5y205d	Caucasian	Post-mortem, death by complications, presumed SUDEP,NICHD Brain and Tissue Bank
78	36	SWS	-	brain	Biol.	No	0.3	12407	43	12450	Amplicon Seq	UMB4731	M	5y205d	Caucasian	Post-mortem, death by complications, presumed SUDEP,NICHD Brain and Tissue Bank
79	36	SWS	-	brain	Biol.	Yes	6.0	13863	890	14753	Amplicon Seq	UMB4731	M	5y205d	Caucasian	Post-mortem, death by complications, presumed SUDEP,NICHD Brain and Tissue Bank
80	36	SWS	-	brain	Biol.	Yes	5.0	12224	639	12863	Amplicon Seq	UMB4731	M	5y205d	Caucasian	Post-mortem, death by complications, presumed SUDEP,NICHD Brain and Tissue Bank
81	36	SWS	-	brain	Biol.	Yes	2.2	16823	378	17201	Amplicon Seq	UMB4731	M	5y205d	Caucasian	Post-mortem, death by complications, presumed SUDEP,NICHD Brain and Tissue Bank
82	37	SWS	-	brain	Biol.	Yes	6.5	13248	919	14167	Amplicon Seq	UMB4812	M	342d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
83	37	SWS	-	brain	Biol.	Yes	5.7	15563	948	16511	Amplicon Seq	UMB4812	M	342d	Caucasian	Surgical tissue NICHD Brain and Tissue Bank
84	38	SWS	-	brain	Biol.	No	0.0	16116	5	16121	Amplicon Seq		M	6y	-	Surgical Tissue
85	38	SWS	-	brain	Biol.	No	0.1	11801	6	11807	Amplicon Seq		M	6y	-	Surgical Tissue
86	39	SWS	-	brain	-	Yes	1.8	32979	615	33594	Amplicon Seq		F	15m	-	Surgical Tissue
87	40	control	-	brain	-	No	0.1	14863	17	14880	Amplicon Seq	UMB1113	M	56y297d	Caucasian	Autopsy NICHD Brain and Tissue Bank
88	41	control	-	brain	-	No	0.0	10168	5	10173	Amplicon Seq	UMB118	F	2y163d	African American	Autopsy NICHD Brain and Tissue Bank
89	42	control	-	brain	-	No	0.1	10025	8	10033	Amplicon Seq	UMB1823	M	15y124d	Caucasian	Autopsy NICHD Brain and Tissue Bank
90	43	control	-	brain	-	No	0.1	12770	12	12782	Amplicon Seq	UMB4104	M	24y	African American	Autopsy NICHD Brain and Tissue Bank
91	44	control	-	brain	-	No	0.0	11108	5	11113	Amplicon Seq	UMB650	F	25y137d	Caucasian	Autopsy NICHD Brain and Tissue Bank
92	45	control	-	brain	-	No	0.0	10959	4	10963	Amplicon Seq	UMB1275	F	2y57d	African American	Autopsy NICHD Brain and Tissue Bank
93	46	CCM	-	brain	-	No	0.0	-	-	-	SNaPshot		-	-	-	Cerebral cavernous malformation
94	47	CCM	-	brain	-	No	0.0	-	-	-	SNaPshot		-	-	-	Cerebral cavernous malformation
95	48	CCM	-	brain	-	No	0.0	-	-	-	SNaPshot		-	-	-	Cerebral cavernous malformation
96	49	CCM	-	brain	-	No	0.0	-	-	-	SNaPshot		-	-	-	Cerebral cavernous malformation

Table S2. Amplicon sequencing primer components.

Primers were designed using sequencing primer and adapter sequences provided by Illumina via private correspondance. P1 and P2 produce a barcoded amplicon containing the sequence of interest. P3 and P4 amplify the product of P1 and P2, and add clustering adapters for Illumina MiSeq flowcells. P1_1 and P1_2 are the 5' and 3' fragments of P1.

Name	Length	Description		Sequence
P1	70	Forward amplicon w/ barcode	5'	ACACTTTCCCTACACGACGCTCTCCGATCTNNNNNNNNNGGTATTGATGATCCCTGTGGTGGG
P2	61	Reverse amplicon	5'	CTCGGCATTCCCTGCTGAACCGCTCTCCGATCTCCTTCCGTAGACAGCTTGATG
P3	58	Sequencing adapter 1	5'	AATGATAACGGCGACCACCGAGATCTACACTTTCCCTACACGACGCTCTCCGATCT
P4	61	Sequencing adapter 2	5'	CAAGCAGAACGACGGCATACGAGATCGGTCTCGGCATTGCTGAACCGCTCTCCGATCT
		P1_1	5'	ACACTTTCCCTACACGACGCTCTCCGATCT
		p1_2	5'	GGGTATTGATGATCCCTGTGGTGGG
		color_balance	5'	GATC
		color_balance	5'	ATCG
		color_balance	5'	TCGA
		color_balance	5'	CGAT

Table S3. Amplicon sequencing primers with barcodes.

Four circularly permuted color balance sequences were added before each barcode sequence to provide an internal measure for fluorescence intensities during base calling. 96 barcoded primer sequences were generated.

Barcode	Name	Lengt	Primer sequence
GATCTTATAAC	P1_1	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCTTATAACGGGTATTGATGATCCCTGTGGTGGG
ATCGTTAATTG	P1_2	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGTTAATTGGGTATTGATGATCCCTGTGGTGGG
TCGAAAGTTT	P1_3	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAAAGTTGGGTATTGATGATCCCTGTGGTGGG
CGATTATTATG	P1_4	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATTATTGGGTATTGATGATCCCTGTGGTGGG
GATCATTAGTT	P1_5	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCATTAGTTGGGTATTGATGATCCCTGTGGTGGG
ATCGATTTAG	P1_6	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCTAGTTAGGGTATTGATGATCCCTGTGGTGGG
TCGATATATGT	P1_7	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATATATGTGGGTATTGATGATCCCTGTGGTGGG
CGATCTATAGT	P1_8	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATCTAGTTGGGTATTGATGATCCCTGTGGTGGG
GATCAAATCCT	P1_9	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCAAATCCTGGGTATTGATGATCCCTGTGGTGGG
ATCGTCAACTA	P1_10	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGCAACTAGGGTATTGATGATCCCTGTGGTGGG
TCGATCATGAT	P1_11	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATCATGATGGGTATTGATGATCCCTGTGGTGGG
CGATCTAACATCA	P1_12	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATCTAACATCAGGGTATTGATGATCCCTGTGGTGGG
GATCAAACCTC	P1_13	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCAAACACTCGGGTATTGATGATCCCTGTGGTGGG
ATCGGGATTT	P1_14	70	5' ACACTTTCCCTACACGACGCTTCCGATCTACGGGATTGGGTATTGATGATCCCTGTGGTGGG
TCGAATCAACT	P1_15	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAACACTGGTATTGATGATCCCTGTGGTGGG
CGATTACCATA	P1_16	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATTACCATAGGGTATTGATGATCCCTGTGGTGGG
GATCTACACAT	P1_17	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCACATGGGTATTGATGATCCCTGTGGTGGG
ATCGATCCTAA	P1_18	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATCTAACAGGGTATTGATGATCCCTGTGGTGGG
TCGATTGCAAT	P1_19	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATTGCAATGGTATTGATGATCCCTGTGGTGGG
CGATTTGGTA	P1_20	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATTGGTAGGGTATTGATGATCCCTGTGGTGGG
GATCCATTACA	P1_21	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCCATTACAGGGTATTGATGATCCCTGTGGTGGG
ATCGACTAAC	P1_22	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGACTAACAGGGTATTGATGATCCCTGTGGTGGG
TCGAGTTGATT	P1_23	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAGTTGGGTATTGATGATCCCTGTGGTGGG
CGATACTTCAA	P1_24	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATACTCAAGGGTATTGATGATCCCTGTGGTGGG
GATCTGTTGTA	P1_25	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCTGTTAGGGTATTGATGATCCCTGTGGTGGG
ATCGCATATAC	P1_26	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGCATATACGGGATTGGGTATTGATGATCCCTGTGGTGGG
TCGATGTTAT	P1_27	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATGTTGATGGGTATTGATGATCCCTGTGGTGGG
CGATGTTTGA	P1_28	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATGTTGAGGGTATTGATGATCCCTGTGGTGGG
GATCCCACAAT	P1_29	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCCCACAATGGGTATTGATGATCCCTGTGGTGGG
ATCGTTAGCCA	P1_30	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGTAGGCCAGGGTATTGATGATCCCTGTGGTGGG
TCGAGAATCTC	P1_31	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAGAATCGGGTATTGATGATCCCTGTGGTGGG
CGATAGACCTT	P1_32	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATAGACCTGGGTATTGATGATCCCTGTGGTGGG
GATCTTACGGT	P1_33	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGATCTACGGTGGGTATTGATGATCCCTGTGGTGGG
ATCGAGATTCC	P1_34	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAGATTCCGGTATTGATGATCCCTGTGGTGGG
TCGAGAACTCT	P1_35	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGAGAACTCGGGTATTGATGATCCCTGTGGTGGG
CGATCCAGTTA	P1_36	70	5' ACACTTTCCCTACACGACGCTTCCGATCTCGATCCAGTTAGGGTATTGATGATCCCTGTGGTGGG
GATCTGCTACA	P1_37	70	5' ACACTTTCCCTACACGACGCTTCCGATCTGCTACAGGGTATTGATGATCCCTGTGGTGGG

ATCGGTCAATC	P1_38	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGGTCAATCGGTATTGATGCCGTGGTGGG
TCGAACCGATT	P1_39	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGAACCGATTGGTATTGATGCCGTGGTGGG
CGATGTCTCAA	P1_40	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATGTCTAAGGGTATTGATGCCGTGGTGGG
GATCCACTGTA	P1_41	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCACTGTAGGGTATTGATGCCGTGGTGGG
ATCGTGCATAC	P1_42	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGTGACACGGTATTGATGCCGTGGTGGG
TCGACACGTAT	P1_43	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACACGTATGGTATTGATGCCGTGGTGGG
CGATACTTGA	P1_44	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATACCTGAGGGTATTGATGCCGTGGTGGG
GATCTCGTAGT	P1_45	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCTGTAGTGGTATTGATGCCGTGGTGGG
ATCGCTGACTA	P1_46	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGCTGACTAGGGTATTGATGCCGTGGTGGG
TCGACTGTGAT	P1_47	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACTGTGATGGTATTGATGCCGTGGTGGG
CGATTGATCA	P1_48	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATTGATCAGGGTATTGATGCCGTGGTGGG
GATCATTGACC	P1_49	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATATTGACCGGGTATTGATGCCGTGGTGGG
ATCGGCTAACT	P1_50	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGGTAACGGTATTGATGCCGTGGTGGG
TCGACGTCATA	P1_51	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACGTACAGGGTATTGATGCCGTGGTGGG
CGATTATGCAC	P1_52	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATTATGACCGGGTATTGATGCCGTGGTGGG
GATCCGTACAT	P1_53	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCGTACAGGGTATTGATGCCGTGGTGGG
ATCGATTCCGA	P1_54	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGATTCCGAGGGTATTGATGCCGTGGTGGG
TCGATATCGCA	P1_55	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATATCGCAGGGTATTGATGCCGTGGTGGG
CGATGCTCTAA	P1_56	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATGCTTAAGGGTATTGATGCCGTGGTGGG
GATCTCACAGC	P1_57	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCTCACAGCGGGTATTGATGCCGTGGTGGG
ATCGCTAGCTG	P1_58	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGCTAGCTGGGTATTGATGCCGTGGTGGG
TCGACTACGAC	P1_59	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACTACGACGGTATTGATGCCGTGGTGGG
CGATTCACTCG	P1_60	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATTGATCAGGGTATTGATGCCGTGGTGGG
GATCCGCTATG	P1_61	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCGTATGGGTATTGATGCCGTGGTGGG
ATCGATCTCGG	P1_62	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGATCTCGGGGTATTGATGCCGTGGTGGG
TCGATACTGCG	P1_63	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATACTCGGGGTATTGATGCCGTGGTGGG
CGATATCGGT	P1_64	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATATCGTCGGGTATTGATGCCGTGGTGGG
GATCGCCAGTT	P1_65	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATGCCAGTGGGTATTGATGCCGTGGTGGG
ATCGGCCTTAG	P1_66	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGGCTTAGGGTATTGATGCCGTGGTGGG
TCGATACGTGC	P1_67	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATACGTGGGTATTGATGCCGTGGTGGG
CGATCGCATGT	P1_68	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATCGATGTGGGTATTGATGCCGTGGTGGG
GATCCGTAAC	P1_69	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCGTAAACGGTATTGATGCCGTGGTGGG
ATCGTTGACCG	P1_70	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGTTGACCGGGTATTGATGCCGTGGTGGG
TCGAAGGTCTC	P1_71	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGAACGGTCTGGGTATTGATGCCGTGGTGGG
CGATGAGCCTT	P1_72	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATGAGCCTGGGTATTGATGCCGTGGTGGG
GATCTTGTGGC	P1_73	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCTTGCGGGTATTGATGCCGTGGTGGG
ATCGGAGTTCC	P1_74	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGGAGTTCCGGTATTGATGCCGTGGTGGG
TCGAAGGCTCT	P1_75	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGAACGGCTCTGGGTATTGATGCCGTGGTGGG
CGATCCGATTG	P1_76	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATCCGATTGGGTATTGATGCCGTGGTGGG
GATCTGTCACG	P1_77	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCTGTACGGGGTATTGATGCCGTGGTGGG
ATCGGTTCCAG	P1_78	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTACGGTTCCAGGGGTATTGATGCCGTGGTGGG
TCGATGTACGC	P1_79	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATGTCACGCGGGTATTGATGCCGTGGTGGG
CGATCATGCGT	P1_80	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATCATGCGTGGGTATTGATGCCGTGGTGGG

GATCGTTAGCC	P1_81	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCGTAGCCGGTATTGATGCCCTGTGGTGGG
ATCGACTGGCT	P1_82	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGACTGGCTGGGTATTGATGCCCTGTGGTGGG
TCGACATCGTG	P1_83	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACATCGTGGGTATTGATGCCCTGTGGTGGG
CGATACTCTGG	P1_84	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATACTCTGGGGTATTGATGCCCTGTGGTGGG
GATCCCACCG	P1_85	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCCCAACCGGGGTATTGATGCCCTGTGGTGGG
ATCGCCATGGC	P1_86	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTATGCCATGGCGGGTATTGATGCCCTGTGGTGGG
TCGACACCACG	P1_87	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACACCACGGGTATTGATGCCCTGTGGTGGG
CGATACCCAG	P1_88	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATACCCAGGGTATTGATGCCCTGTGGTGGG
GATCCACACGC	P1_89	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCCACACGCGGGTATTGATGCCCTGTGGTGGG
ATCGTGGCGT	P1_90	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTATCGTGGCGTGGGTATTGATGCCCTGTGGTGGG
TCGAACCAGCC	P1_91	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGAACCAAGCCGGGTATTGATGCCCTGTGGTGGG
CGATGTGGCT	P1_92	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATGTCGGCTGGGTATTGATGCCCTGTGGTGGG
GATCTGCCGTG	P1_93	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTGATCTGCCGTGGGTATTGATGCCCTGTGGTGGG
ATCGGTCCCTGG	P1_94	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTATCGGTCCCTGGGGTATTGATGCCCTGTGGTGGG
TCGACTGCAGC	P1_95	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGACTGCAGCGGGTATTGATGCCCTGTGGTGGG
CGATAAGCCCC	P1_96	70	5'	ACACTCTTCCCTACACGACGCTCTCCGATCTCGATAAGCCCCGGGTATTGATGCCCTGTGGTGGG

Table S4. Targeted mutagenesis primer sequences.

GNAQ R183Q SDM pos G>A	5'	ATGTGCTTAGAGTTCAAGTCCCCACCAAGGGA
GNAQ R183Q SDM neg G>A	5'	CCTGTGGTGGGGACTTGAACTCTAACGCACATC
GNAQ Q209L SDM pos A>T	5'	GTCGATGTAGGGGCCTAAGGTCAGAGAGAAG
GNAQ Q209L SDM neg A>T	5'	CTTCTCTCTGACCTTAGGCCCTACATCGAC

Table S5. SNaPshot primer sequences.

GNAQ exon 4 amplicon forward and reverse primers produce a 207bp amplicon containing the sequence of interest. Primers for single base pair extension (SNaPshot) are designed immediately upstream and downstream of the base of interest, c.548G>A.

GNAQ exon 4 amplicon		Primer sequence
Forward	5'	ATTGTGTCTTCCCTCCTCTA
Reverse	5'	GGTTTCATGGACTCAGTTAC
SNaPshot Forward	5'	CGCAACAAGATGTGCTTAGAGTTC
SNaPshot Reverse	5'	TCCCTGTGGTGGGACT

GNA11 exon 4 amplicon forward and reverse primers produce a 207bp amplicon containing the sequences of interest. Primers for single base pair extension (SNaPshot) are designed immediately upstream and downstream of the bases of interest, c.547C>T, c.546C>T, and c.548G>A.

GNA11 exon 4 amplicon		Primer sequence
Forward	5'	GAGCACCCACCGCTGTGTTG
Reverse	5'	GGCAAATGAGCCTCTCAGTGC
SNaPshot Forward 1 (547C>T)	5'	CAGGACGTGCTGCCGGTC
SNaPshot Reverse 1 (547C>T)	5'	TGCCGGTGGTGGGCACGC
SNaPshot Forward 2 (546C>T)	5'	GCAGGACGTGCTGCCGGGT
SNaPshot Forward 3 (548G>A)	5'	AGGACGTGCTGCCGGTCC
SNaPshot Reverse 3 (548G>A)	5'	ATGCCGGTGGTGGCACCG

GNA11 exon 5 amplicon forward and reverse primers produce a 189bp amplicon containing the sequences of interest. Primers for single base pair extension (SNaPshot) are designed immediately upstream and downstream of the bases of interest, c.626A>T or C and c. 627G>A or T.

GNA11 exon 5 amplicon		Primer sequence
Forward	5'	GTCCTGGGATTGCAGATTG
Reverse	5'	GACCAAGTCCTGGTGGAGTC
SNaPshot Forward 1 (626A>T, C)	5'	GGTGGATGTGGGGGGCC
SNaPshot Reverse 1 (626A>T, C)	5'	TCCTCCGCTCCGACCGC
SNaPshot Reverse 2 (627G>A, T)	5'	TTCCTCCGCTCCGACCG

Table S6. Somatic variants detected in paired affected whole genome sequence.

Variants called somatic in affected genomes by Strelka.¹ Coordinates are hg19. Allele frequencies are for alternate allele. Non-synonymous variants are bold.

				Subject 1						Subject 2						Subject 3					
hg19 coordinates		Alleles		Unaffected			Affected			Unaffected			Affected			Unaffected			Affected		
Chromosome	Position	Ref	Alt	Freq	Alt	Ref	Freq	Alt	Ref	Freq	Alt	Ref	Freq	Alt	Ref	Freq	Alt	Ref	Freq	Alt	Ref
chr1	101237270	A	C	10.3	4	35	24.1	13	41	31.8	7	15	19.0	4	17	45.7	21	25	48.4	15	16
chr1	103650463	C	A	4.8	2	40	20.0	9	36	3.4	1	28	0.0	0	27	0.0	0	39	0.0	0	31
chr1	103650465	C	G	4.7	2	41	15.9	7	37	0.0	0	29	0.0	0	28	0.0	0	39	0.0	0	31
chr1	117152010	C	T	2.2	1	45	18.2	8	36	5.9	2	32	12.5	4	28	18.5	10	44	3.7	1	26
chr1	117152011	A	G	2.1	1	46	20.0	9	36	5.9	2	32	9.4	3	29	17.9	10	46	3.6	1	27
chr1	120190829	C	T	5.0	1	19	21.1	4	15	3.6	1	27	20.0	7	28	17.9	5	23	27.8	5	13
chr1	120389866	G	A	9.3	5	49	6.7	5	70	8.6	3	32	2.7	1	36	2.1	1	46	8.0	4	46
chr1	121357337	T	A	2.5	5	199	1.6	4	243	0.6	1	175	5.1	9	168	1.8	4	217	2.4	5	202
chr1	121357410	C	A	2.1	8	382	3.4	14	396	2.0	7	348	5.4	21	366	2.8	12	420	5.2	22	399
chr1	121367371	T	C	1.4	1	69	1.3	1	79	1.0	2	191	4.4	8	174	3.9	5	123	1.2	1	82
chr1	121403291	C	A	0.0	0	89	0.0	0	90	0.0	0	43	10.3	6	52	5.2	3	55	1.9	1	52
chr1	12890038	A	C	0.0	0	51	17.8	8	37	0.0	0	44	5.0	2	38	28.2	11	28	23.3	7	23
chr1	12927186	G	A	4.5	2	42	2.7	1	36	6.9	2	27	0.0	0	29	0.0	0	23	30.0	9	21
chr1	13915474	T	G	26.7	16	44	21.5	14	51	21.1	8	30	22.2	8	28	0.0	0	39	0.0	0	42
chr1	13915475	A	T	26.7	16	44	22.7	15	51	21.6	8	29	21.6	8	29	0.0	0	38	0.0	0	42
chr1	142557366	T	C	0.0	0	52	0.0	0	56	0.0	0	40	7.8	4	47	3.1	2	62	4.5	4	84
chr1	142577273	A	G	1.3	2	154	0.9	2	209	3.6	6	163	7.5	14	173	2.7	8	293	5.0	11	208
chr1	142581371	A	T	2.2	2	91	2.2	2	91	0.9	1	111	5.6	6	102	5.3	10	180	4.2	6	138
chr1	142583601	C	T	0.0	0	74	0.0	0	90	0.0	0	144	0.0	0	112	0.0	0	193	6.7	11	153
chr1	142587118	G	C	2.5	3	117	6.9	9	121	4.4	3	65	1.9	2	102	0.7	1	142	5.7	9	150
chr1	142591858	A	G	6.0	10	157	3.7	6	156	1.9	3	152	3.2	6	180	2.9	8	267	3.4	8	224
chr1	142594490	A	T	7.7	9	108	2.0	2	98	1.1	1	87	6.1	6	93	0.0	0	150	5.6	7	119
chr1	142623619	T	C	0.6	1	164	0.5	1	193	0.0	0	78	6.4	6	88	1.3	2	155	1.5	2	132
chr1	142638441	G	A	0.9	1	109	7.3	11	140	15.7	14	75	9.5	10	95	15.8	26	139	14.9	18	103
chr1	142639470	G	C	0.0	0	188	0.0	0	185	1.0	1	98	8.5	9	97	4.9	9	174	7.1	11	143
chr1	142641015	A	G	0.0	0	71	8.0	7	81	1.1	1	91	0.0	0	86	1.4	2	145	1.1	1	92
chr1	142644958	C	T	6.7	12	167	4.4	8	172	4.4	6	130	6.6	11	155	6.2	16	244	6.2	14	211
chr1	142650124	T	G	9.1	17	169	6.5	13	188	0.0	0	117	0.0	0	126	1.0	2	202	5.2	9	163
chr1	142660660	C	T	7.1	22	289	7.4	23	287	0.0	0	92	0.0	0	144	1.6	3	189	5.9	11	175
chr1	142664497	A	T	0.0	0	112	0.0	0	111	0.0	0	65	8.0	7	80	2.9	3	101	4.3	4	90
chr1	142671854	C	G	2.1	7	328	1.2	4	317	0.0	0	91	1.5	2	130	0.0	0	174	3.8	6	150
chr1	142721870	T	C	11.3	12	94	13.6	19	121	8.3	6	66	3.6	3	81	0.9	1	108	8.8	6	62
chr1	142822532	C	T	2.5	3	118	5.5	8	137	2.6	2	76	6.1	6	92	0.6	1	169	5.2	8	146
chr1	142903725	T	C	1.0	1	98	0.0	0	89	5.1	2	37	1.9	1	52	0.0	0	99	5.7	5	83
chr1	142906610	T	C	7.2	9	116	13.0	16	107	0.0	0	53	8.3	7	77	6.5	10	144	6.6	8	113
chr1	142966193	A	G	7.1	3	39	4.8	3	60	6.7	5	70	11.7	11	83	10.0	14	126	8.7	10	105
chr1	143120732	G	A	1.6	1	62	5.2	3	55	7.3	3	38	10.0	5	45	0.0	0	68	15.5	9	49

				Subject 1							Subject 2							Subject 3						
chr1	143120843	T	C	8.2	15	167	12.0	23	169	2.3	2	86	11.0	12	97	0.7	1	145	7.0	9	120			
chr1	143123138	C	T	0.0	0	111	8.1	10	113	6.7	6	83	8.0	7	81	11.2	15	119	15.7	19	102			
chr1	143145418	G	A	8.8	6	62	0.0	0	61	2.1	2	95	9.9	9	82	6.5	6	87	7.9	5	58			
chr1	143151018	A	G	0.9	1	111	3.7	5	131	2.0	2	97	12.1	13	94	4.1	6	142	10.4	14	121			
chr1	143153736	T	C	26.9	25	68	31.5	23	50	24.0	12	38	21.4	12	44	11.1	6	48	24.4	10	31			
chr1	143176467	G	A	3.9	6	149	6.1	9	138	3.5	2	55	10.7	8	67	5.4	6	106	6.3	5	74			
chr1	143183513	C	T	19.1	13	55	22.7	15	51	0.0	0	41	11.5	6	46	14.1	9	55	14.1	10	61			
chr1	143184097	G	A	3.3	5	145	3.2	6	179	1.0	1	98	6.9	8	108	2.7	5	179	4.8	8	160			
chr1	143184101	G	C	3.4	5	141	4.0	7	170	1.0	1	97	7.0	8	107	2.2	4	175	4.8	8	158			
chr1	143184125	T	C	5.3	9	162	7.3	15	190	0.9	1	105	9.3	11	107	2.7	5	177	7.7	12	143			
chr1	143205361	G	A	14.1	9	55	8.6	6	64	3.8	2	50	9.3	4	39	2.0	1	50	25.6	11	32			
chr1	143234905	C	A	24.1	14	44	32.1	18	38	0.0	0	31	13.7	7	44	10.2	10	88	5.6	4	68			
chr1	143241963	T	C	3.8	4	101	6.1	8	124	8.4	9	98	4.3	4	90	1.0	1	98	8.6	10	106			
chr1	143248682	G	C	3.1	2	63	4.8	2	40	3.2	1	30	36.4	20	35	23.9	11	35	24.1	14	44			
chr1	143249090	G	A	6.5	10	143	11.4	18	140	8.8	16	165	11.1	17	136	3.3	6	176	6.7	10	140			
chr1	143258006	C	T	0.0	0	70	7.4	6	75	15.2	16	89	6.3	6	90	4.5	5	105	10.7	12	100			
chr1	143258014	C	T	0.0	0	79	8.2	8	90	15.1	19	107	7.3	8	101	5.4	8	140	8.1	11	125			
chr1	143349339	A	T	0.0	0	49	1.5	1	65	4.7	3	61	12.5	7	49	0.0	0	78	16.9	10	49			
chr1	143386513	G	A	1.1	2	185	2.8	6	208	3.2	4	122	2.1	3	142	1.7	3	176	6.1	9	138			
chr1	143395394	G	C	6.1	5	77	3.1	3	94	0.0	0	65	7.1	5	65	4.4	3	65	3.2	2	61			
chr1	143395412	T	C	5.5	5	86	2.8	3	106	0.0	0	69	7.0	5	66	7.2	5	64	4.2	3	68			
chr1	143398505	G	T	4.8	15	298	3.7	12	311	2.7	4	143	5.5	11	188	1.8	4	220	5.7	13	215			
chr1	143427356	C	G	0.0	0	203	0.0	0	222	3.6	4	106	5.9	8	128	0.0	0	154	4.1	5	117			
chr1	143445752	C	T	1.7	2	119	1.7	3	174	2.1	4	185	8.7	13	136	3.7	9	233	3.7	7	180			
chr1	143465402	T	C	0.0	0	143	0.0	0	146	5.2	3	55	6.0	6	94	5.5	6	103	4.7	4	82			
chr1	143480104	T	A	0.0	0	42	2.2	1	45	1.5	1	67	7.8	5	59	0.0	0	67	8.1	7	79			
chr1	143482141	C	T	9.4	17	163	10.2	17	150	0.0	0	108	5.8	7	114	4.1	6	142	3.5	5	138			
chr1	143491919	G	A	0.4	1	237	0.0	0	279	2.1	3	139	4.3	7	156	1.1	2	181	5.5	9	156			
chr1	143499006	C	T	1.1	1	91	0.0	0	99	5.0	8	151	3.4	5	142	0.0	0	171	8.0	10	115			
chr1	143510777	T	C	2.0	3	149	2.3	4	167	1.0	1	96	1.9	2	101	0.7	1	149	5.6	7	118			
chr1	143514925	C	A	10.9	14	115	16.3	27	139	1.4	2	139	8.6	14	149	5.3	12	214	6.3	10	150			
chr1	143519255	A	T	3.8	6	151	0.5	1	202	1.6	3	180	0.8	1	132	1.0	2	207	4.4	7	151			
chr1	145052366	A	C	9.7	7	65	21.7	13	47	0.0	0	28	24.1	7	22	10.3	4	35	12.8	5	34			
chr1	146472785	T	C	21.8	12	43	12.8	6	41	0.0	0	34	26.8	11	30	29.9	20	47	20.0	8	32			
chr1	148514467	G	A	2.2	1	45	20.8	10	38	26.5	9	25	21.9	7	25	16.9	10	49	11.1	5	40			
chr1	148847308	T	G	2.0	3	148	3.8	6	154	1.6	2	123	1.2	2	160	1.0	2	198	7.1	14	183			
chr1	148847582	T	A	1.0	1	98	1.9	2	103	3.4	4	112	0.0	0	96	4.3	7	155	6.6	8	113			
chr1	148853628	C	T	9.0	19	193	11.3	19	149	3.9	3	74	14.1	18	110	7.0	9	120	10.3	12	105			
chr1	148871079	T	C	3.8	6	153	6.0	11	171	3.0	4	129	7.3	11	139	1.7	3	177	5.9	10	160			
chr1	149026785	T	C	10.3	8	70	14.3	9	54	0.0	0	91	6.2	5	76	7.4	7	88	9.2	7	69			
chr1	149698233	G	A	3.3	2	58	6.5	4	58	0.0	0	23	0.0	0	28	0.0	0	44	15.4	6	33			
chr1	156079613	A	G	1.7	1	58	6.1	4	62	3.4	1	28	0.0	0	34	40.0	10	15	64.3	18	10			
chr1	156858051	T	C	34.7	26	49	36.5	23	40	45.0	9	11	35.4	17	31	23.1	9	30	29.3	12	29			
chr1	157555130	C	T	0.0	0	40	9.1	5	50	2.6	1	38	10.8	4	33	8.1	3	34	5.1	2	37			
chr1	157555134	C	T	9.8	4	37	5.8	3	49	0.0	0	38	16.7	6	30	2.8	1	35	0.0	0	40			
chr1	157730480	A	G	0.0	0	49	0.0	0	42	0.0	0	26	20.0	6	24	2.9	1	33	0.0	0	43			
chr1	166029355	G	T	0.0	0	46	0.0	0	55	0.0	0	33	0.0	0	42	0.0	0	47	12.9	4	27			

				Subject 1						Subject 2						Subject 3					
chr1	167132395	C	A	8.1	5	57	6.3	4	60	0.0	0	28	0.0	0	36	0.0	0	31	0.0	0	37
chr1	167978591	T	C	2.3	1	43	0.0	0	24	0.0	0	17	23.5	8	26	9.1	3	30	20.0	7	28
chr1	16842292	G	C	19.6	41	168	28.4	67	169	1.9	2	101	5.3	8	143	17.6	31	145	18.5	27	119
chr1	16908582	T	G	0.0	0	151	0.0	0	134	10.9	5	41	12.5	7	49	0.0	0	96	9.3	8	78
chr1	17054920	A	T	2.9	4	133	2.1	3	138	0.0	0	96	1.0	1	103	1.2	2	171	3.5	5	138
chr1	17054921	A	T	2.9	4	133	1.4	2	137	0.0	0	97	0.0	0	105	1.2	2	170	4.2	6	136
chr1	17190953	G	T	0.0	0	48	0.0	0	50	0.0	0	35	0.0	0	24	0.0	0	34	10.8	4	33
chr1	17218658	T	C	0.0	0	76	0.0	0	72	0.0	0	26	6.1	2	31	1.3	1	77	11.7	7	53
chr1	174164750	T	C	0.0	0	21	0.0	0	28	0.0	0	28	13.2	5	33	0.0	0	38	0.0	0	28
chr1	17518395	T	C	2.9	1	34	12.9	4	27	0.0	0	27	21.7	5	18	32.3	10	21	52.6	10	9
chr1	175729196	G	A	0.0	0	60	1.6	1	62	2.5	1	39	8.3	4	44	4.2	2	46	3.1	1	31
chr1	184437147	A	T	0.0	0	48	9.8	4	37	24.1	7	22	31.0	13	29	0.0	0	33	0.0	0	41
chr1	185624971	A	G	3.4	1	28	20.0	8	32	0.0	0	38	0.0	0	20	0.0	0	36	0.0	0	43
chr1	196721234	T	C	2.1	1	47	8.9	4	41	0.0	0	37	17.9	10	46	12.5	9	63	19.7	12	49
chr1	20129411	A	T	0.0	0	5	0.0	0	5	3.8	1	25	23.5	8	26	36.4	8	14	18.8	3	13
chr1	202565424	C	T	0.0	0	48	0.0	0	46	0.0	0	11	0.0	0	23	9.5	4	38	22.6	7	24
chr1	203872968	T	G	0.0	0	52	0.0	0	44	0.0	0	44	0.0	0	29	0.0	0	51	9.8	5	46
chr1	204164502	T	C	11.6	18	137	10.9	13	106	0.0	0	42	12.5	6	42	6.1	4	62	13.7	7	44
chr1	21773444	G	C	0.0	0	56	0.0	0	51	3.6	1	27	17.5	7	33	3.0	1	32	0.0	0	47
chr1	218519392	G	A	0.0	0	61	0.0	0	68	9.4	3	29	19.5	8	33	0.0	0	37	0.0	0	26
chr1	22696670	C	T	66.7	4	2	75.0	3	1	0.0	0	22	25.0	5	15	3.6	1	27	0.0	0	27
chr1	228315094	C	T	5.0	2	38	26.1	12	34	0.0	0	23	0.0	0	27	20.0	7	28	9.7	3	28
chr1	232448358	G	T	16.7	7	35	29.5	13	31	0.0	0	36	0.0	0	41	22.2	10	35	22.9	8	27
chr1	242481829	A	G	1.8	1	55	12.3	7	50	6.9	2	27	4.3	1	22	1.9	1	52	3.6	1	27
chr1	246415225	C	T	0.0	0	61	0.0	0	45	0.0	0	23	0.0	0	22	0.0	0	18	28.0	7	18
chr1	246438872	T	C	0.0	0	30	25.0	12	36	87.5	7	1	57.9	11	8	12.9	4	27	15.0	3	17
chr1	246438878	G	T	0.0	0	32	16.7	8	40	30.8	4	9	38.1	8	13	0.0	0	31	5.6	1	17
chr1	247926367	A	T	68.8	11	5	85.7	18	3	74.2	23	8	0	25	0	89.7	26	3	87.2	34	5
chr1	248646341	A	T	0.0	0	40	0.0	0	58	2.3	1	42	0.0	0	32	0.0	0	45	13.0	6	40
chr1	30703007	T	C	1.8	1	56	1.9	1	53	7.1	2	26	17.6	6	28	0.0	0	31	0.0	0	27
chr1	3093083	C	T	0.0	0	93	0.0	0	79	0.0	0	42	10.0	4	36	4.5	2	42	9.1	3	30
chr1	31249254	G	A	2.6	1	38	9.8	4	37	4.8	1	20	0.0	0	22	0.0	0	31	0.0	0	30
chr1	31973133	C	G	32.0	24	51	29.1	23	56	38.2	13	21	38.2	13	21	65.9	29	15	52.2	12	11
chr1	37012430	A	G	0.0	0	30	9.1	4	40	14.3	4	24	16.1	5	26	0.0	0	26	0.0	0	29
chr1	37012492	A	G	11.1	5	40	8.5	4	43	0.0	0	30	11.9	5	37	0.0	0	31	0.0	0	32
chr1	39195377	A	G	31.7	13	28	27.1	13	35	20.6	7	27	34.9	15	28	15.6	5	27	16.1	5	26
chr1	55310655	T	G	0.0	0	24	14.3	6	36	0.0	0	28	0.0	0	33	0.0	0	29	0.0	0	24
chr1	569878	C	G	15.8	15	80	65.9	147	76	36.7	22	38	69.1	65	29	81.3	226	52	87.3	213	31
chr1	5733653	T	C	4.1	2	47	15.0	6	34	0.0	0	28	21.2	7	26	8.6	5	53	11.1	5	40
chr1	5733654	G	A	4.1	2	47	17.9	7	32	0.0	0	29	21.2	7	26	8.5	5	54	11.4	5	39
chr1	58019182	G	A	17.1	6	29	28.6	12	30	26.7	8	22	23.5	8	26	5.1	2	37	31.3	15	33
chr1	67301897	G	A	0.0	0	34	0.0	0	31	5.0	1	19	3.7	1	26	0.0	0	23	19.4	7	29
chr1	727913	A	G	27.3	12	32	19.2	10	42	2.5	1	39	20.0	9	36	23.3	17	56	32.0	16	34
chr1	727962	T	C	19.4	6	25	14.0	8	49	0.0	0	42	11.6	5	38	19.2	14	59	32.7	16	33
chr1	7559336	G	T	5.6	4	68	2.7	2	71	13.0	3	20	15.2	5	28	0.0	0	23	27.6	8	21
chr1	7559354	G	A	8.9	7	72	15.1	11	62	11.5	3	23	13.8	4	25	0.0	0	27	30.0	9	21
chr1	79195002	T	G	29.6	16	38	47.5	19	21	19.2	10	42	17.8	8	37	11.5	6	46	7.9	3	35

				Subject 1						Subject 2						Subject 3						
chr1	815160	T	C	0.0	0	58	0.0	0	84	0.0	0	75	5.1	5	93	2.6	3	113	1.7	2	113	
chr1	815892	A	G	1.8	1	54	1.9	1	52	2.4	2	83	1.2	1	81	0.8	1	127	3.9	4	98	
chr1	81815324	C	T	35.9	14	25	42.6	23	31	38.5	10	16	37.9	11	18	0.0	0	45	0.0	0	35	
chr1	83711121	A	G	0.0	0	39	0.0	0	36	0.0	0	36	17.8	8	37	0.0	0	51	0.0	0	32	
chr1	91610902	C	T	8.7	2	21	21.3	10	37	55.2	16	13	63.0	17	10	0.0	0	52	0.0	0	41	
chr1	91703656	G	T	57.9	22	16	39.5	17	26	9.8	4	37	15.9	7	37	23.8	15	48	23.5	8	26	
chr1	99888959	T	C	20.0	5	20	31.3	10	22	50.0	15	15	52.4	11	10	19.4	7	29	18.2	4	18	
chr2	104382974	T	C	0	2	0	60.0	6	4	32.4	12	25	35.3	6	11	50.0	18	18	50.0	11	11	
chr2	1107710	G	A	0.0	0	68	6.3	4	60	14.3	6	36	15.7	8	43	0.0	0	45	4.7	2	41	
chr2	1107734	T	A	0.0	0	78	5.3	4	71	2.8	1	35	3.6	2	53	0.0	0	40	2.3	1	43	
chr2	112323644	T	C	5.5	3	52	0.0	0	34	0.0	0	31	15.8	6	32	20.0	5	20	17.8	8	37	
chr2	112335685	C	T	0.0	0	17	0.0	0	12	8.7	2	21	17.2	5	24	4.2	1	23	22.2	4	14	
chr2	114196356	A	G	0.0	0	39	10.3	4	35	0.0	0	36	0.0	0	25	0.0	0	57	0.0	0	39	
chr2	114327456	A	G	6.8	3	41	18.6	11	48	3.2	1	30	24.5	12	37	8.9	5	51	13.7	7	44	
chr2	114407300	T	A	0.0	0	43	0.0	0	39	30.0	6	14	14.3	2	12	3.8	1	25	31.8	7	15	
chr2	117104162	A	G	0.0	0	32	16.0	4	21	36.4	8	14	56.3	9	7	3.0	1	32	0.0	0	27	
chr2	124219094	T	C	3.6	1	27	12.5	5	35	44.4	8	10	32.1	9	19	41.2	14	20	48.4	15	16	
chr2	124542162	C	T	0.0	0	14	2.9	1	34	6.7	2	28	18.2	4	18	0.0	0	37	9.1	4	40	
chr2	131003967	A	T	3.4	3	86	1.1	1	87	0.0	0	38	10.5	4	34	3.6	2	54	4.3	2	45	
chr2	132106942	A	G	0.0	0	40	12.1	4	29	0.0	0	34	0.0	0	35	6.1	3	46	7.0	3	40	
chr2	132112841	C	A	0.0	0	66	6.8	5	69	0.0	0	29	0.0	0	40	0.0	0	42	0.0	0	39	
chr2	132112877	C	T	0.0	0	47	8.3	5	55	0.0	0	25	0.0	0	34	0.0	0	47	0.0	0	39	
chr2	132129774	C	T	5.0	2	38	12.0	6	44	3.4	1	28	9.1	2	20	0.0	0	54	12.5	5	35	
chr2	132531591	T	G	5.9	1	16	5.0	2	38	3.1	1	31	8.7	2	21	0.0	0	25	18.5	5	22	
chr2	132539498	C	A	0.0	0	37	20.7	6	23	6.5	3	43	13.0	3	20	0.0	0	49	0.0	0	32	
chr2	132542578	C	T	6.3	4	60	7.7	5	60	2.8	1	35	22.9	8	27	7.3	4	51	10.3	4	35	
chr2	132549406	A	G	12.8	6	41	18.0	9	41	15.4	4	22	10.7	3	25	0.0	0	37	10.9	5	41	
chr2	132708075	A	G	17.3	9	43	16.9	10	49	0.0	0	34	15.7	8	43	10.9	5	41	7.5	3	37	
chr2	132771549	A	G	2.6	6	222	4.7	11	222	4.1	9	208	4.2	9	205	4.7	14	285	6.9	15	203	
chr2	132776610	T	C	0.0	0	72	8.8	6	62	0.0	0	0	55	0.0	0	50	0.0	0	63	0.0	0	54
chr2	132788860	A	G	2.8	1	35	2.3	1	42	5.9	2	32	16.7	4	20	0.0	0	48	14.8	4	23	
chr2	132831650	G	A	13.7	7	44	21.8	17	61	4.2	1	23	21.6	11	40	13.7	7	44	15.6	7	38	
chr2	132839250	C	T	0.0	0	49	2.0	1	48	7.1	2	26	5.7	2	33	0.0	0	50	19.5	8	33	
chr2	132848551	C	A	0.0	0	36	0.0	0	30	0.0	0	26	20.0	5	20	0.0	0	37	0.0	0	24	
chr2	132944113	G	A	9.4	3	29	13.9	5	31	11.1	5	40	14.8	4	23	3.5	2	55	21.1	8	30	
chr2	133111417	A	G	7.1	6	79	6.0	5	78	9.6	5	47	3.1	2	63	1.1	1	87	6.2	5	76	
chr2	133112059	C	G	3.0	3	97	5.3	6	108	0.0	0	67	6.9	4	54	2.0	2	96	2.7	2	71	
chr2	139955893	A	T	0.0	0	44	0.0	0	28	0.0	0	28	0.0	0	32	5.4	2	35	16.7	6	30	
chr2	150178553	C	T	0.0	0	44	7.7	4	48	0.0	0	34	0.0	0	35	4.1	2	47	3.6	2	53	
chr2	15057088	G	A	0.0	0	77	0.0	0	68	0.0	0	37	10.6	5	42	0.0	0	59	0.0	0	50	
chr2	156259884	C	G	0.0	0	30	0.0	0	44	0.0	0	29	0.0	0	23	14.3	5	30	24.3	9	28	
chr2	156259886	C	G	0.0	0	31	0.0	0	44	0.0	0	28	0.0	0	23	14.7	5	29	25.7	9	26	
chr2	157653508	A	G	0.0	0	54	0.0	0	80	0.0	0	34	0.0	0	34	13.6	6	38	29.8	14	33	
chr2	157653509	A	C	0.0	0	54	0.0	0	80	0.0	0	34	2.9	1	33	14.0	6	37	29.2	14	34	
chr2	157753561	G	T	28.6	10	25	36.8	14	24	26.5	9	25	31.0	9	20	37.3	22	37	33.3	12	24	
chr2	1626031	G	C	0.0	0	116	0.8	1	120	0.0	0	34	0.0	0	46	0.0	0	23	35.3	6	11	
chr2	164817451	A	G	13.5	5	32	13.2	5	33	8.0	2	23	0.0	0	26	20.8	11	42	16.7	8	40	

				Subject 1						Subject 2						Subject 3					
chr2	16912850	C	T	3.1	1	31	4.8	2	40	0.0	0	29	0.0	0	33	6.0	3	47	18.9	7	30
chr2	173398199	T	G	21.7	13	47	24.4	11	34	14.3	4	24	26.5	9	25	4.1	2	47	6.1	2	31
chr2	178524785	T	C	0.0	0	32	0.0	0	46	0.0	0	35	17.2	5	24	0.0	0	37	0.0	0	33
chr2	19683026	A	T	7.7	1	12	36.4	4	7	6.0	3	47	3.6	1	27	0.0	0	40	8.2	4	45
chr2	199318776	T	C	0.0	0	39	0.0	0	38	0.0	0	24	21.2	7	26	22.6	7	24	17.0	8	39
chr2	202971967	T	A	13.3	6	39	18.9	10	43	26.2	11	31	15.4	8	44	20.8	10	38	11.9	5	37
chr2	204831784	G	A	12.0	3	22	9.1	3	30	0.0	0	26	0.0	0	36	0.0	0	21	38.1	8	13
chr2	233304524	G	A	0.0	0	71	0.0	0	50	0.0	0	33	18.2	6	27	2.2	1	44	0.0	0	28
chr2	235379041	T	C	0.0	0	38	11.4	5	39	0.0	0	26	0.0	0	43	6.8	3	41	5.5	3	52
chr2	241099194	A	T	0.0	0	33	0.0	0	33	17.2	5	24	20.8	5	19	0.0	0	37	0.0	0	27
chr2	241099195	T	A	0.0	0	33	2.9	1	33	17.2	5	24	20.0	5	20	0.0	0	36	0.0	0	27
chr2	243153118	C	T	0.0	0	99	0.0	0	96	2.9	1	33	25.4	15	44	0.0	0	30	0.0	0	38
chr2	3332735	A	G	13.0	6	40	21.7	10	36	0.0	0	31	4.2	1	23	0.0	0	21	16.7	4	20
chr2	34924009	C	A	20.0	6	24	50.0	23	23	0.0	0	22	33.3	10	20	2.0	1	49	0.0	0	37
chr2	52163242	A	G	0.0	0	19	0.0	0	17	3.3	1	29	5.0	1	19	0.0	0	29	15.6	5	27
chr2	57458121	G	T	0.0	0	70	0.0	0	73	0.0	0	19	38.1	8	13	2.4	1	40	0.0	0	35
chr2	57709688	G	A	72.2	13	5	87.5	7	1	25.0	1	3	85.7	6	1	0.0	0	18	36.4	4	7
chr2	60840539	G	A	25.0	4	12	23.1	6	20	13.8	4	25	13.8	4	25	0.0	0	40	32.0	8	17
chr2	70518146	A	C	2.9	1	34	22.6	7	24	46.2	12	14	32.1	9	19	0.0	0	28	0.0	0	15
chr2	7104204	C	A	1.3	1	77	8.7	6	63	0.0	0	42	0.0	0	51	0.0	0	73	0.0	0	39
chr2	73877086	C	T	19.4	6	25	10.2	5	44	0.0	0	30	15.2	5	28	15.8	6	32	16.7	6	30
chr2	740840	G	T	7.0	13	173	7.0	13	172	5.0	1	19	0.0	0	23	0.0	0	88	9.2	6	59
chr2	8232346	G	A	8.1	3	34	9.4	5	48	12.2	5	36	22.6	7	24	0.0	0	49	2.1	1	46
chr2	82365421	T	C	4.2	2	46	2.9	1	33	27.6	8	21	42.4	14	19	35.0	14	26	36.6	15	26
chr2	85225719	C	T	0.0	0	18	21.2	7	26	0.0	0	25	0.0	0	22	0.0	0	39	0.0	0	27
chr2	87593187	C	A	0.0	0	79	7.1	7	92	8.8	6	62	4.6	3	62	1.7	2	117	7.4	7	88
chr2	87620726	A	G	0.0	0	10	0.0	0	11	15.8	6	32	20.0	7	28	3.1	2	62	18.3	11	49
chr2	88160577	T	G	2.8	1	35	0.0	0	40	2.4	1	41	12.5	5	35	0.0	0	95	1.5	1	64
chr2	88169524	A	G	0.0	0	36	12.5	7	49	9.8	4	37	12.5	4	28	7.5	4	49	13.0	7	47
chr2	89072533	G	T	8.0	7	80	8.3	7	77	6.0	3	47	15.9	10	53	7.2	6	77	11.3	8	63
chr2	89082118	G	A	0.0	0	61	0.0	0	62	2.5	1	39	11.9	5	37	10.9	7	57	15.0	9	51
chr2	89102821	C	T	0.0	0	61	9.2	6	59	8.7	9	94	8.6	8	85	7.9	12	140	19.2	20	84
chr2	90403713	T	C	5.7	2	33	0.0	0	57	2.6	1	37	8.6	3	32	0.0	0	43	7.4	4	50
chr2	90408215	G	C	0.0	0	135	0.0	0	148	1.9	2	102	8.4	9	98	5.9	7	111	5.6	7	119
chr2	91918762	G	A	1.8	2	111	8.7	9	94	0.0	0	60	11.5	7	54	9.0	12	121	2.2	2	87
chr2	92036200	T	A	0.0	0	34	4.0	1	24	8.0	2	23	4.3	1	22	0.0	0	47	16.2	6	31
chr2	92064609	T	C	16.7	9	45	27.1	13	35	0.0	0	32	8.8	3	31	0.0	0	35	20.5	8	31
chr2	92091909	A	T	0.0	0	41	2.6	1	38	0.0	0	32	13.5	5	32	6.3	3	45	4.7	2	41
chr2	92103970	T	G	0.0	0	27	20.0	6	24	0.0	0	18	0.0	0	16	4.7	2	41	13.6	3	19
chr2	92103973	C	A	0.0	0	28	20.7	6	23	0.0	0	18	0.0	0	15	4.9	2	39	13.6	3	19
chr2	92121387	T	C	6.8	5	69	5.6	3	51	2.6	1	37	10.3	6	52	20.2	18	71	17.7	11	51
chr2	92121402	T	A	1.4	1	69	3.6	2	53	2.4	1	40	8.1	5	57	16.3	14	72	6.7	4	56
chr2	92154532	G	A	0.0	0	146	0.0	0	144	3.6	3	80	7.5	7	86	3.0	3	96	1.0	1	103
chr2	92191547	A	T	0.0	0	53	17.2	10	48	9.5	4	38	8.9	5	51	7.3	6	76	11.4	5	39
chr2	92239112	T	C	0.0	0	56	0.0	0	61	2.3	1	42	0.0	0	42	2.1	1	46	9.3	4	39
chr2	92265487	T	C	1.8	6	322	2.9	8	269	0.7	1	136	6.1	10	155	3.4	6	171	3.0	5	160
chr2	92285765	G	A	9.0	8	81	7.8	8	94	1.2	1	81	5.0	4	76	0.8	1	117	7.5	8	99

				Subject 1							Subject 2							Subject 3							
chr2	92304867	G	T	6.7	2	28	24.4	11	34	12.5	7	49	10.8	7	58	17.9	12	55	37.0	17	29				
chr2	92319961	T	C	0.4	2	449	2.5	13	502	17.6	181	850	16.6	149	749	18.7	266	1155	19.5	248	1021				
chr2	92325501	G	A	1.8	5	271	5.6	16	268	1.2	3	251	3.2	17	516	2.9	26	870	2.8	31	1058				
chr2	92325799	A	G	0.1	1	760	0.2	2	818	0.6	3	531	1.1	6	548	0.5	5	908	3.4	31	874				
chr2	95369116	G	C	1.7	1	59	0.0	0	67	0.0	0	34	2.6	1	38	0.0	0	49	8.5	5	54				
chr2	95440553	A	G	9.8	4	37	37.8	14	23	0.0	0	26	2.4	1	41	0.0	0	41	2.0	1	49				
chr2	95474559	C	A	0.0	0	14	0.0	0	29	10.7	3	25	4.2	1	23	5.9	2	32	24.3	9	28				
chr2	95511866	C	T	4.3	3	66	2.5	2	79	6.8	5	69	15.6	12	65	4.6	7	144	6.0	7	110				
chr2	95536638	T	C	1.0	1	96	9.4	8	77	14.6	6	35	22.2	12	42	26.8	19	52	32.1	18	38				
chr2	95554455	G	T	1.6	1	61	6.2	4	61	0.0	0	43	13.1	8	53	6.3	5	74	8.3	6	66				
chr2	95554467	G	T	1.5	1	64	3.3	2	59	0.0	0	42	7.9	5	58	6.4	5	73	9.2	7	69				
chr2	95554514	A	C	0.0	0	66	0.0	0	73	0.0	0	49	7.1	5	65	4.7	4	81	6.8	5	68				
chr2	95565856	C	T	18.8	9	39	25.7	9	26	17.1	6	29	10.6	5	42	0.0	0	41	17.3	9	43				
chr2	95569196	T	C	0.0	0	71	8.6	6	64	28.8	21	52	29.9	20	47	21.4	15	55	27.0	20	54				
chr2	97839762	C	G	2.3	1	42	8.9	4	41	20.0	10	40	28.6	10	25	23.9	16	51	20.9	14	53				
chr2	97845973	A	G	14.5	12	71	7.9	6	70	0.0	0	54	13.0	7	47	12.5	9	63	15.2	7	39				
chr2	9861127	A	G	1.8	1	55	6.8	4	55	0.0	0	27	0.0	0	46	2.0	1	49	2.6	1	37				
chr3	105874363	C	T	20.0	8	32	30.0	15	35	0	41	0	0	26	0	15.8	6	32	24.4	10	31				
chr3	109417	A	G	6.1	2	31	19.4	12	50	0.0	0	38	0.0	0	34	0.0	0	48	0.0	0	35				
chr3	111517529	A	T	25.0	6	18	35.0	7	13	31.1	14	31	29.4	10	24	34.1	15	29	27.3	12	32				
chr3	116266452	G	A	11.4	4	31	18.5	5	22	20.0	6	24	30.0	9	21	15.4	8	44	15.4	4	22				
chr3	122214109	C	A	48.4	15	16	36.0	9	16	14.6	6	35	19.4	6	25	17.6	6	28	29.5	13	31				
chr3	125627118	G	A	1.7	1	58	4.7	2	41	3.4	1	28	4.7	2	41	0.0	0	52	15.6	5	27				
chr3	129770349	C	T	0.0	0	44	7.5	4	49	0.0	0	7	0.0	0	14	5.9	1	16	0.0	0	14				
chr3	129824571	G	A	1.9	1	51	7.0	4	53	0.0	0	24	0.0	0	37	2.0	1	48	2.9	1	34				
chr3	129824583	A	G	1.9	1	51	9.3	5	49	0.0	0	30	0.0	0	35	2.2	1	45	2.6	1	38				
chr3	129864617	C	T	6.5	2	29	5.3	1	18	0.0	0	21	25.0	6	18	8.0	2	23	0.0	0	18				
chr3	129864619	A	T	3.7	1	26	13.0	3	20	4.8	1	20	28.0	7	18	11.5	3	23	10.0	2	18				
chr3	129930939	C	G	0.0	0	27	0.0	0	30	0.0	0	10	0.0	0	23	0.0	0	24	17.4	4	19				
chr3	131334796	A	C	0.0	0	59	0.0	0	61	0.0	0	26	5.4	2	35	0.0	0	53	18.4	7	31				
chr3	141024204	G	A	10.5	4	34	18.5	10	44	21.9	7	25	21.1	8	30	19.6	9	37	39.5	15	23				
chr3	1426498	T	C	58.8	10	7	58.3	14	10	0.0	0	33	16.7	4	20	4.0	1	24	0.0	0	23				
chr3	145785451	A	T	18.4	9	40	22.6	14	48	39.5	15	23	13.6	3	19	0.0	0	45	2.5	1	39				
chr3	149940821	T	C	15.7	8	43	24.6	14	43	23.3	7	23	31.4	11	24	26.1	12	34	40.5	17	25				
chr3	15100527	T	A	1.8	1	55	13.0	7	47	2.8	1	35	3.1	1	31	9.8	4	37	3.0	1	32				
chr3	166472635	C	A	51.6	16	15	55.0	22	18	0.0	0	34	0.0	0	42	0.0	0	58	0.0	0	34				
chr3	176468850	C	A	16.3	7	36	11.6	5	38	0.0	0	27	12.9	4	27	2.0	1	48	0.0	0	36				
chr3	176509087	G	A	0.0	0	28	9.5	2	19	0.0	0	18	2.8	1	35	0.0	0	28	20.7	6	23				
chr3	179185821	A	T	20.0	1	4	12.5	1	7	16.2	6	31	19.4	7	29	0.0	0	50	0.0	0	31				
chr3	179185823	A	T	33.3	2	4	22.2	2	7	16.2	6	31	20.0	7	28	0.0	0	49	0.0	0	29				
chr3	193893984	A	G	0.0	0	32	0.0	0	43	0.0	0	22	0.0	0	32	18.8	9	39	48.1	13	14				
chr3	193893989	A	G	0.0	0	30	0.0	0	44	0.0	0	27	0.0	0	32	19.6	9	37	48.1	13	14				
chr3	195230277	A	G	0.0	0	199	0.0	0	215	1.9	1	53	14.8	12	69	5.8	11	180	9.5	16	153				
chr3	195230290	T	G	2.9	6	201	6.6	14	198	1.9	1	51	10.3	8	70	8.3	16	177	13.7	24	151				
chr3	195412832	T	C	21.0	13	49	20.6	14	54	0.0	0	22	22.9	8	27	10.3	6	52	11.1	6	48				
chr3	195412864	G	A	22.8	13	44	32.8	20	41	0.0	0	24	28.1	9	23	11.1	6	48	12.5	6	42				
chr3	195689849	A	G	2.8	1	35	0.0	0	38	0.0	0	21	26.7	8	22	12.5	5	35	4.9	2	39				

				Subject 1						Subject 2						Subject 3					
chr3	197382706	T	C	0.0	0	90	0.0	0	96	1.8	1	56	9.5	7	67	8.7	8	84	12.1	8	58
chr3	197836711	C	A	0.0	0	42	4.8	3	60	2.3	1	43	2.8	1	35	0.0	0	49	9.8	4	37
chr3	197841278	G	C	0.0	0	39	9.4	5	48	7.1	4	52	3.3	2	59	4.5	3	63	5.0	2	38
chr3	197854901	T	C	0.0	0	50	0.0	0	44	0.0	0	67	7.3	6	76	2.4	3	123	7.0	6	80
chr3	197895865	T	A	2.4	13	533	1.7	10	585	1.8	6	334	0.8	3	373	1.1	7	613	2.3	12	521
chr3	28906906	T	C	2.5	1	39	8.3	4	44	0.0	0	46	0.0	0	36	0.0	0	39	0.0	0	39
chr3	28975641	C	T	13.2	7	46	12.3	7	50	0.0	0	19	17.4	4	19	0.0	0	35	0.0	0	30
chr3	35581328	A	T	0.0	0	2	0	1	0	27.0	10	27	40.0	16	24	0.0	0	23	28.2	11	28
chr3	36260911	C	G	26.2	11	31	10.0	6	54	10.0	4	36	24.2	8	25	2.2	1	45	10.9	6	49
chr3	46383613	C	T	0.0	0	39	0.0	0	46	0.0	0	34	7.1	4	52	0.0	0	59	0.0	0	35
chr3	58981700	A	C	13.6	6	38	14.3	8	48	10.5	6	51	17.6	6	28	7.1	3	39	13.9	5	31
chr3	60015627	G	C	3.6	2	53	23.4	11	36	18.2	4	18	17.4	8	38	0.0	0	32	0.0	0	35
chr3	70695822	T	C	0.0	0	18	0.0	0	13	83.3	20	4	65.5	19	10	0.0	0	28	20.0	6	24
chr3	75446338	C	T	4.8	2	40	2.0	1	48	2.8	1	35	0.0	0	40	0.0	0	25	15.8	3	16
chr3	75513913	A	T	0.0	0	55	14.0	6	37	0.0	0	32	0.0	0	30	0.0	0	26	0.0	0	20
chr3	75657316	A	G	5.3	2	36	19.5	8	33	6.5	2	29	16.0	4	21	0.0	0	36	21.3	10	37
chr3	75658564	G	A	1.8	1	54	4.2	3	68	0.0	0	24	2.9	1	34	0.0	0	45	9.8	4	37
chr3	75702813	T	C	0.0	0	64	0.0	0	80	0.0	0	53	0.0	0	56	1.1	1	86	10.8	7	58
chr3	75702836	T	C	0.0	0	74	0.0	0	92	0.0	0	62	0.0	0	66	1.1	1	87	9.8	8	74
chr3	75723091	A	G	1.4	2	146	3.7	6	158	7.6	13	159	5.4	9	157	6.4	16	235	6.0	13	202
chr3	75745467	A	G	6.3	7	105	7.4	11	137	1.1	2	173	3.9	8	198	6.5	15	216	5.3	11	195
chr3	75820861	G	A	0.0	0	56	10.0	6	54	10.0	4	36	0.0	0	52	3.8	2	51	9.5	4	38
chr3	75848889	A	C	16.1	5	26	20.9	9	34	0.0	0	36	12.5	5	35	4.1	3	71	6.7	3	42
chr3	75851055	G	C	12.0	3	22	5.1	2	37	3.2	1	30	7.9	3	35	0.0	0	41	10.9	5	41
chr3	75860303	A	G	11.9	8	59	13.9	10	62	0.0	0	45	12.2	6	43	1.5	1	65	6.0	4	63
chr3	75862770	T	A	0.0	0	33	4.5	2	42	0.0	0	55	8.0	4	46	3.7	2	52	5.0	3	57
chr3	75867897	A	G	0.0	0	42	0.0	0	48	4.2	1	23	10.2	5	44	0.0	0	56	10.9	6	49
chr3	75870398	A	G	2.5	1	39	2.6	1	38	0.0	0	38	19.0	8	34	1.6	1	60	5.1	2	37
chr3	75909930	C	A	0.0	0	37	0.0	0	46	2.3	1	43	0.0	0	32	0.0	0	83	8.7	4	42
chr3	75909938	T	C	0.0	0	34	0.0	0	48	2.1	1	46	0.0	0	28	0.0	0	77	7.7	4	48
chr3	75992297	T	G	0.0	0	52	0.0	0	54	0.0	0	40	0.0	0	28	0.0	0	46	7.0	4	53
chr3	79601151	A	C	0.0	0	25	19.5	8	33	0.0	0	30	0.0	0	21	2.4	1	40	2.8	1	35
chr3	81282681	A	G	0.0	0	49	9.8	5	46	0.0	0	26	0.0	0	31	0.0	0	55	0.0	0	42
chr3	87696950	C	T	6.9	2	27	9.5	4	38	0.0	0	26	20.7	6	23	8.6	3	32	6.7	2	28
chr3	87696951	T	C	6.9	2	27	9.8	4	37	0.0	0	26	18.5	5	22	8.6	3	32	6.7	2	28
chr3	99858459	A	G	0.0	0	26	7.9	3	35	0.0	0	20	0.0	0	35	0.0	0	25	6.1	2	31
chr4	103856812	C	A	5.7	3	50	11.1	5	40	3.6	1	27	13.0	3	20	0.0	0	38	22.5	9	31
chr4	109794715	T	C	28.6	16	40	25.8	17	49	27.3	9	24	42.9	18	24	29.3	12	29	21.6	11	40
chr4	112193031	T	A	6.3	2	30	27.5	19	50	18.4	7	31	6.3	2	30	0.0	0	55	0.0	0	54
chr4	115306184	T	A	7.4	2	25	16.1	5	26	3.4	1	28	10.3	3	26	0.0	0	16	0.0	0	20
chr4	119394228	T	A	4.9	2	39	3.2	1	30	0.0	0	33	11.1	4	32	2.9	1	33	2.9	1	33
chr4	122035428	T	C	18.2	8	36	21.3	10	37	25.9	7	20	16.7	7	35	12.7	7	48	23.4	11	36
chr4	12739052	T	C	0.0	0	42	8.3	4	44	2.2	1	45	0.0	0	29	0.0	0	39	0.0	0	44
chr4	129223147	G	T	26.9	14	38	25.5	12	35	14.8	4	23	29.6	8	19	16.3	7	36	26.5	9	25
chr4	132591899	G	C	1.6	1	63	9.1	6	60	2.9	1	34	0.0	0	27	4.9	2	39	3.0	1	32
chr4	132626234	G	A	9.8	6	55	9.9	8	73	0.0	0	65	7.1	5	65	4.3	4	90	4.8	4	79
chr4	132626239	G	T	21.9	14	50	30.2	26	60	0.0	0	62	9.5	7	67	21.6	19	69	34.9	30	56

				Subject 1						Subject 2						Subject 3					
chr4	132865273	T	C	0.0	0	50	14.6	7	41	13.5	5	32	10.7	3	25	8.0	4	46	6.3	2	30
chr4	137859693	C	G	0.0	0	51	9.4	6	58	19.2	5	21	25.9	7	20	40.0	16	24	14.3	4	24
chr4	138103424	T	G	0.0	0	36	9.3	4	39	0.0	0	35	0.0	0	25	1.9	1	52	0.0	0	46
chr4	143727927	A	G	3.2	1	30	2.3	1	42	0.0	0	25	20.7	6	23	8.7	2	21	25.0	10	30
chr4	144793278	A	G	0.0	0	59	0.0	0	48	5.9	2	32	7.3	3	38	0.0	0	43	13.3	6	39
chr4	144793280	C	T	0.0	0	60	0.0	0	45	5.9	2	32	4.9	2	39	0.0	0	48	13.3	6	39
chr4	144793288	C	T	0.0	0	59	0.0	0	43	6.1	2	31	5.3	2	36	0.0	0	48	13.3	6	39
chr4	144793325	A	G	0.0	0	47	0.0	0	53	2.9	1	34	0.0	0	33	0.0	0	55	8.7	4	42
chr4	144843993	T	A	0.0	0	29	0.0	0	39	0.0	0	28	18.2	4	18	0.0	0	48	0.0	0	22
chr4	144936702	T	C	2.9	1	33	0.0	0	20	0.0	0	34	0.0	0	30	0.0	0	58	10.3	4	35
chr4	145037531	C	A	0.0	0	20	0.0	0	21	0.0	0	26	12.5	4	28	13.0	3	20	13.8	4	25
chr4	145047441	C	T	0.0	0	30	0.0	0	29	0.0	0	21	13.6	3	19	3.3	1	29	15.4	4	22
chr4	146879022	T	C	22.2	4	14	0.0	0	23	11.5	3	23	9.4	3	29	0.0	0	30	27.3	9	24
chr4	149429971	G	A	0.0	0	127	0.0	0	118	0.0	0	40	0.0	0	26	0.0	0	51	17.9	7	32
chr4	158533205	T	C	0.0	0	39	13.2	5	33	0.0	0	26	0.0	0	30	2.3	1	42	13.8	4	25
chr4	164591536	G	A	0.0	0	23	22.7	5	17	0.0	0	36	0.0	0	30	30.2	13	30	31.3	10	22
chr4	172034145	A	G	13.6	6	38	20.0	6	24	0.0	0	21	26.1	6	17	50.0	22	22	38.1	16	26
chr4	185141166	G	A	27.7	13	34	23.3	7	23	18.2	4	18	27.3	6	16	14.8	4	23	27.5	11	29
chr4	185141194	A	G	23.7	9	29	19.2	5	21	9.1	2	20	20.8	5	19	0.0	0	28	19.5	8	33
chr4	185473328	T	C	0.0	0	32	9.5	4	38	2.6	1	38	3.1	1	31	0.0	0	45	0.0	0	44
chr4	185755579	T	A	5.0	1	19	10.0	3	27	3.1	1	31	0.0	0	33	19.2	5	21	37.5	9	15
chr4	187129705	C	T	0.0	0	73	8.2	6	67	0.0	0	40	0.0	0	28	0.0	0	38	0.0	0	41
chr4	187129721	A	G	0.0	0	67	11.6	8	61	0.0	0	34	0.0	0	26	0.0	0	39	0.0	0	37
chr4	190608019	G	A	0.0	0	76	1.1	1	86	12.9	4	27	8.3	3	33	0.0	0	55	10.4	5	43
chr4	190608029	G	C	0.0	0	72	2.5	2	79	16.0	4	21	15.6	5	27	0.0	0	51	14.3	6	36
chr4	190758008	C	T	7.0	6	80	14.9	17	97	0.0	0	7	0.0	0	6	0.0	0	1	'NA'	'NA'	'NA'
chr4	190809287	G	A	1.2	1	81	0.0	0	71	0.0	0	36	2.8	1	35	0.0	0	35	12.5	6	42
chr4	190819669	A	G	3.0	2	64	0.0	0	68	0.0	0	53	10.0	6	54	6.5	6	86	1.5	1	65
chr4	190825997	G	T	1.7	4	235	5.8	14	227	3.1	3	94	8.4	12	131	5.4	10	175	1.7	3	172
chr4	190827623	G	T	4.3	4	89	2.9	3	102	1.7	1	58	5.9	4	64	4.3	4	90	4.5	3	64
chr4	190829257	A	G	2.4	1	41	5.8	4	65	0.0	0	62	9.5	6	57	1.1	1	87	1.2	1	84
chr4	190832129	G	A	0.0	0	97	0.0	0	113	0.0	0	92	4.5	5	106	2.8	4	138	3.1	4	124
chr4	190838621	G	A	5.4	12	211	3.1	7	216	2.9	2	67	8.4	10	109	4.2	5	113	2.8	3	103
chr4	190867215	G	C	20.0	8	32	14.8	8	46	0.0	0	32	16.0	8	42	13.0	9	60	23.4	11	36
chr4	190867227	C	T	18.6	8	35	10.9	6	49	0.0	0	29	12.2	5	36	6.7	4	56	11.9	5	37
chr4	190871320	G	T	1.8	3	166	1.3	2	150	7.1	9	117	3.8	5	128	1.1	2	178	5.6	10	170
chr4	190878052	A	C	8.3	3	33	3.0	1	32	2.4	1	40	2.8	1	35	0.0	0	38	9.8	5	46
chr4	190879863	T	C	0.0	0	57	10.0	7	63	19.7	13	53	17.7	11	51	19.8	21	85	12.3	10	71
chr4	190891344	G	T	10.8	8	66	14.3	12	72	2.6	1	38	10.4	5	43	6.6	4	57	1.8	1	55
chr4	190891992	A	G	2.9	3	101	3.9	5	122	2.1	1	46	3.3	2	59	0.0	0	86	8.9	5	51
chr4	190910694	G	A	1.4	1	72	0.0	0	78	5.9	7	111	5.2	6	109	1.5	2	129	5.6	8	134
chr4	190910704	T	A	1.2	1	80	0.0	0	96	5.3	7	126	3.3	4	116	1.5	2	132	5.2	8	145
chr4	190927035	G	T	2.5	3	116	2.8	4	141	5.3	4	71	2.7	3	107	0.0	0	130	5.2	6	110
chr4	190929090	G	T	0.0	0	51	0.0	0	57	7.3	3	38	2.8	1	35	0.0	0	58	13.2	5	33
chr4	190934269	T	C	1.9	5	255	6.5	16	230	3.0	5	161	5.8	12	195	1.1	3	259	5.0	11	209
chr4	190934270	G	T	3.7	10	258	6.9	17	228	1.8	3	164	5.3	11	197	0.8	2	262	5.9	13	208
chr4	190934486	G	A	0.5	1	186	1.6	3	186	0.7	1	147	6.7	11	153	4.8	9	179	10.2	15	132

				Subject 1						Subject 2						Subject 3					
chr4	190935186	C	A	8.5	10	108	7.7	10	120	1.4	2	139	5.1	8	148	1.2	3	249	2.4	4	161
chr4	190969182	G	A	3.7	1	26	7.1	2	26	0.0	0	17	28.0	7	18	41.7	10	14	45.5	5	6
chr4	190971845	T	C	0.0	0	106	0.0	0	113	0.0	0	88	0.0	0	115	1.1	2	188	4.1	6	141
chr4	22625219	T	C	8.3	4	44	5.9	3	48	4.2	1	23	15.4	6	33	2.3	1	42	10.7	3	25
chr4	33838220	T	A	2.2	1	45	13.0	6	40	14.0	6	37	4.3	2	45	4.8	2	40	13.2	7	46
chr4	33862849	T	C	17.8	13	60	19.7	14	57	0.0	0	41	19.6	10	41	19.6	11	45	26.7	12	33
chr4	33864560	G	A	3.6	2	54	6.7	3	42	0.0	0	33	13.5	5	32	1.6	1	62	9.1	4	40
chr4	34009180	T	C	0.0	0	30	0.0	0	41	0.0	0	34	7.8	4	47	2.0	1	50	0.0	0	57
chr4	38330318	C	T	7.9	3	35	9.5	4	38	11.9	5	37	26.7	8	22	0.0	0	47	0.0	0	30
chr4	4044576	C	T	0.0	0	38	0.0	0	46	0.0	0	34	13.0	7	47	11.1	6	48	14.9	7	40
chr4	4228418	G	A	0.0	0	81	0.0	0	60	2.6	1	38	18.2	10	45	2.1	1	47	2.3	1	43
chr4	4234227	G	A	0.0	0	22	0.0	0	29	3.8	1	25	4.5	1	21	0.0	0	25	14.3	4	24
chr4	45029450	A	T	3.6	2	54	3.2	2	61	3.2	1	30	0.0	0	39	0.0	0	44	10.5	6	51
chr4	49102374	C	G	0.0	0	648	0.7	5	735	0.7	2	271	2.2	7	307	0.9	3	314	0.4	1	279
chr4	49112529	C	T	0.0	0	658	0.5	4	730	1.4	5	354	2.8	11	382	1.4	8	552	0.4	2	505
chr4	49116905	C	G	1.5	2	129	1.3	2	152	6.9	5	67	1.9	2	103	2.1	2	93	5.2	5	92
chr4	49159383	A	T	0.7	1	141	5.5	10	173	0.0	0	153	0.0	0	137	6.3	13	194	2.6	4	149
chr4	49160190	T	C	1.0	2	201	2.9	7	236	7.9	16	187	6.2	13	197	7.2	18	232	13.7	26	164
chr4	49166006	G	A	0.0	0	323	0.3	1	324	0.8	1	126	9.0	15	151	3.8	9	228	4.2	8	183
chr4	49170548	C	G	0.0	0	60	1.5	1	65	4.3	2	45	5.5	3	52	0.0	0	43	11.7	7	53
chr4	49186587	G	T	0.0	0	53	11.3	6	47	13.2	7	46	16.3	7	36	5.4	6	105	6.9	6	81
chr4	49193209	C	G	0.0	0	34	0.0	0	33	4.5	1	21	11.1	3	24	0.0	0	28	15.6	5	27
chr4	49214844	T	C	3.0	3	97	3.2	3	92	3.1	2	63	9.4	8	77	16.1	22	115	10.2	9	79
chr4	49244264	G	T	0.0	0	37	0.0	0	41	8.6	3	32	11.1	5	40	2.3	1	43	16.0	8	42
chr4	49247526	C	T	1.8	1	54	18.2	12	54	5.7	5	83	11.5	12	92	7.2	7	90	11.7	7	53
chr4	49251110	G	A	1.8	2	109	2.1	2	94	3.3	2	58	3.5	3	82	1.1	1	93	9.9	10	91
chr4	49251760	G	A	1.1	3	260	0.7	2	267	1.6	2	120	4.9	9	176	1.4	3	210	1.7	4	228
chr4	49270617	C	T	4.5	5	106	5.9	8	127	0.0	0	83	7.2	10	129	10.6	17	143	11.1	17	136
chr4	49273630	T	A	0.0	0	369	0.0	0	352	10.4	17	146	8.9	19	194	2.2	5	226	3.5	9	251
chr4	49321651	A	C	6.9	7	94	7.7	9	108	0.8	1	121	4.1	6	141	1.7	3	172	5.6	9	152
chr4	49324185	G	T	0.0	0	66	0.0	0	59	0.0	0	52	8.3	6	66	0.0	0	43	0.0	0	31
chr4	49497862	T	C	1.9	2	105	5.0	6	113	0.0	0	121	6.2	8	121	4.0	6	144	5.2	7	127
chr4	49524324	G	A	0.0	0	43	0.0	0	41	5.9	3	48	4.4	2	43	1.0	1	98	10.4	8	69
chr4	49549492	G	A	0.0	0	33	0.0	0	36	10.0	4	36	12.7	7	48	1.3	1	79	6.3	4	59
chr4	49549821	A	G	0.0	0	103	2.2	2	91	0.0	0	60	3.0	2	64	1.2	1	80	6.3	4	60
chr4	49586596	C	T	2.1	1	46	6.9	2	27	8.8	3	31	8.3	3	33	0.0	0	43	9.6	5	47
chr4	49590201	T	C	1.0	1	104	0.9	1	113	2.4	1	41	11.1	7	56	0.0	0	47	4.4	2	43
chr4	55199774	G	A	23.5	12	39	25.9	15	43	0.0	0	28	0.0	0	37	16.7	10	50	14.3	5	30
chr4	57084616	C	G	17.4	4	19	13.8	4	25	18.5	5	22	6.7	1	14	0.0	0	29	15.6	5	27
chr4	66441714	G	A	0.0	0	23	18.9	7	30	0.0	0	21	0.0	0	15	8.3	2	22	3.7	1	26
chr4	69880204	A	G	13.5	5	32	20.0	7	28	14.0	6	37	15.2	5	28	3.1	2	62	13.2	5	33
chr4	69880208	A	C	13.2	5	33	20.0	7	28	14.3	6	36	14.7	5	29	1.6	1	61	14.3	5	30
chr4	70087418	A	T	8.8	6	62	8.6	6	64	0.0	0	29	13.5	5	32	13.8	8	50	11.6	5	38
chr4	70087439	A	G	10.8	7	58	15.8	12	64	0.0	0	36	15.4	6	33	14.8	9	52	15.2	7	39
chr4	70138129	A	T	9.7	3	28	14.3	4	24	0.0	0	36	14.5	8	47	7.8	4	47	11.6	5	38
chr4	7685105	G	A	2.3	1	42	21.1	8	30	6.7	1	14	4.8	1	20	38.5	5	8	27.3	3	8
chr4	79987926	A	G	0.0	0	43	6.7	5	70	2.0	1	49	0.0	0	45	0.0	0	58	2.6	1	38

				Subject 1							Subject 2							Subject 3						
chr4	80837018	A	C	50.0	9	9	53.6	15	13	0.0	0	21	5.3	1	18	0.0	0	36	0.0	0	28			
chr4	82324170	G	A	0.0	0	34	0.0	0	22	0.0	0	19	27.3	9	24	0.0	0	17	0.0	0	29			
chr4	82324182	A	G	17.9	7	32	4.2	1	23	4.3	1	22	20.0	6	24	27.8	5	13	22.6	7	24			
chr4	85465092	C	A	13.7	7	44	33.3	17	34	20.7	6	23	24.4	10	31	47.5	29	32	38.5	15	24			
chr4	9640573	G	C	2.2	1	45	1.5	1	66	0.0	0	25	13.3	4	26	12.2	5	36	5.9	2	32			
chr4	96933796	G	A	0.0	0	31	0.0	0	36	50.0	12	12	38.7	12	19	3.1	1	31	5.4	2	35			
chr4	9720037	A	T	14.5	8	47	25.5	14	41	8.7	2	21	21.6	11	40	14.3	8	48	11.4	4	31			
chr4	99772084	A	G	0.0	0	20	3.0	1	32	0.0	0	20	20.0	5	20	0.0	0	22	0.0	0	18			
chr5	106735078	A	G	0.0	0	65	1.4	1	71	0.0	0	39	15.8	6	32	0.0	0	40	2.2	1	45			
chr5	113642398	T	C	0.0	0	27	2.6	1	37	3.8	1	25	39.1	9	14	0.0	0	40	0.0	0	27			
chr5	123297937	G	A	40.5	17	25	40.9	18	26	46.4	13	15	29.6	8	19	8.5	4	43	27.5	11	29			
chr5	127849719	G	A	21.3	10	37	18.8	13	56	7.7	3	36	9.5	4	38	0.0	0	51	0.0	0	42			
chr5	134263676	G	A	0.0	0	63	15.4	10	55	10.3	3	26	10.9	5	41	40.3	25	37	26.6	17	47			
chr5	134263712	A	G	0.0	0	56	20.7	12	46	18.5	5	22	9.5	4	38	36.8	21	36	22.0	11	39			
chr5	138481355	G	A	0.0	0	31	7.5	3	37	0.0	0	23	0.0	0	24	4.8	2	40	22.2	6	21			
chr5	1396749	A	T	0.0	0	66	0.0	0	63	0.0	0	22	0.0	0	33	0.0	0	35	10.4	5	43			
chr5	144160425	C	T	0.0	0	44	0.0	0	44	12.9	4	27	20.0	9	36	8.9	5	51	24.4	10	31			
chr5	145268735	A	G	0.0	0	25	23.3	7	23	14.3	2	12	9.1	2	20	16.0	4	21	8.3	3	33			
chr5	166172669	C	T	12.0	3	22	11.1	5	40	4.5	1	21	16.7	5	25	14.3	5	30	17.9	5	23			
chr5	167169988	C	A	7.4	4	50	3.4	2	56	0.0	0	25	0.0	0	46	17.5	7	33	35.5	11	20			
chr5	173888667	G	A	15.0	6	34	20.0	7	28	2.9	1	34	14.6	7	41	0.0	0	34	5.0	2	38			
chr5	18254780	C	T	5.6	3	51	10.3	4	35	0.0	0	31	7.1	3	39	11.1	6	48	3.1	1	31			
chr5	20926755	T	C	2.9	1	33	10.5	4	34	0.0	0	30	0.0	0	36	2.9	1	34	14.3	6	36			
chr5	21479291	A	G	15.3	19	105	18.3	20	89	0.0	0	53	0.0	0	73	0.0	0	50	7.9	5	58			
chr5	236734	G	C	4.8	4	79	3.7	3	79	0.0	0	52	9.8	6	55	2.0	1	50	0.0	0	44			
chr5	265784	C	A	21.4	9	33	17.9	7	32	0.0	0	18	29.2	7	17	8.9	4	41	9.7	3	28			
chr5	265810	A	C	20.9	9	34	15.2	7	39	0.0	0	21	26.1	6	17	12.2	5	36	12.9	4	27			
chr5	265822	T	C	20.0	8	32	17.8	8	37	0.0	0	21	23.8	5	16	10.8	4	33	10.0	3	27			
chr5	32560132	A	G	55.6	10	8	36.8	7	12	57.1	4	3	72.7	8	3	20.0	4	16	60.0	18	12			
chr5	49435265	C	G	0.6	3	464	3.0	14	451	14.2	43	260	7.5	22	270	3.9	17	418	2.2	9	401			
chr5	49435703	T	C	4.4	23	502	3.7	18	463	1.9	5	252	1.3	5	366	1.8	10	549	4.6	25	522			
chr5	49439315	C	T	0.0	0	29	0.0	0	37	0.0	0	116	3.6	5	132	4.1	7	164	5.9	8	128			
chr5	68013720	G	C	0.0	0	47	12.8	5	34	0.0	0	34	0.0	0	39	0.0	0	45	0.0	0	38			
chr5	68759455	T	A	0.0	0	2	0.0	0	5	4.2	2	46	15.6	5	27	2.6	1	37	15.6	7	38			
chr5	82596398	C	T	8.3	2	22	19.2	5	21	35.0	7	13	51.5	17	16	44.4	16	20	31.4	11	24			
chr5	82596399	C	G	9.5	2	19	25.0	5	15	23.1	3	10	34.8	8	15	52.0	13	12	36.4	8	14			
chr5	98132052	A	C	20.7	6	23	33.3	11	22	40.9	9	13	37.5	12	20	53.8	21	18	41.7	15	21			
chr5	98823378	G	T	0.0	0	29	17.6	6	28	4.5	1	21	0.0	0	16	22.2	6	21	14.3	3	18			
chr5	98823382	G	C	0.0	0	30	25.7	9	26	0.0	0	21	0.0	0	17	22.2	6	21	20.0	4	16			
chr6	1053878	A	G	2.6	3	113	1.8	2	112	11.5	3	23	3.9	2	49	0.0	0	52	7.7	4	48			
chr6	11491236	C	G	22.2	22	77	26.4	32	89	8.3	2	22	8.8	3	31	12.0	6	44	9.1	4	40			
chr6	134796938	T	C	0.0	0	13	0.0	0	5	0.0	0	18	0.0	0	18	0.0	0	19	20.0	5	20			
chr6	136963234	T	A	0.0	0	28	0.0	0	27	0.0	0	50	11.1	5	40	6.3	2	30	5.4	2	35			
chr6	14179314	A	G	0.0	0	93	0.0	0	86	0.0	0	27	0.0	0	49	0.0	0	42	0.0	0	37			
chr6	145198682	A	T	0.0	0	40	22.5	9	31	0.0	0	22	0.0	0	32	5.6	2	34	0.0	0	34			
chr6	146889414	A	T	23.5	16	52	21.0	13	49	4.3	1	22	33.3	12	24	37.8	14	23	41.7	10	14			
chr6	150267934	A	G	2.1	1	47	0.0	0	46	0.0	0	20	17.1	7	34	19.6	11	45	28.6	10	25			

				Subject 1							Subject 2							Subject 3						
				G	A	9.1	2	20	10.3	3	26	40.0	8	12	26.7	8	22	0.0	0	23	34.3	12	23	
chr6	15144633	G	A	9.1	2	20	10.3	3	26	40.0	8	12	26.7	8	22	0.0	0	23	34.3	12	23			
chr6	156880253	T	A	7.8	5	59	5.2	3	55	11.1	3	24	16.7	8	40	0.0	0	51	16.7	9	45			
chr6	157734170	C	A	2.7	14	509	3.2	18	553	1.8	3	163	5.4	10	176	5.0	13	246	3.4	8	225			
chr6	158721666	A	G	11.9	7	52	7.3	3	38	3.3	1	29	7.0	3	40	0.0	0	60	13.3	8	52			
chr6	169465845	A	G	0.0	0	36	11.4	4	31	0.0	0	32	0.0	0	51	0.0	0	64	0.0	0	41			
chr6	170182532	T	C	3.8	1	25	26.7	8	22	0.0	0	16	0.0	0	9	0.0	0	14	0.0	0	11			
chr6	170454419	C	T	3.3	4	119	3.6	4	107	12.5	2	14	4.3	1	22	0.0	0	38	14.7	5	29			
chr6	170486012	G	A	16.0	12	63	14.9	10	57	0.0	0	37	15.1	8	45	2.9	2	68	3.0	2	65			
chr6	170805400	G	A	0.0	0	64	8.3	6	66	0.0	0	19	0.0	0	21	5.3	1	18	15.4	2	11			
chr6	171020919	A	G	0.0	0	99	7.1	7	91	'NA'	'NA'	'NA'	'NA'	'NA'	'NA'	'NA'	'NA'	0	1	0	0	1	0	
chr6	26226628	A	T	4.8	1	20	0.0	0	10	0.0	0	18	0.0	0	24	9.1	3	30	27.8	10	26			
chr6	30980943	G	T	21.2	7	26	25.7	9	26	0.0	0	30	7.4	2	25	4.3	1	22	47.6	10	11			
chr6	30980972	C	T	22.0	11	39	30.2	13	30	0.0	0	32	0.0	0	30	0.0	0	23	40.9	9	13			
chr6	31241338	G	A	0.0	0	41	9.6	5	47	0.0	0	45	0.0	0	43	2.2	1	45	6.1	2	31			
chr6	3472702	G	A	35.3	18	33	41.4	24	34	12.5	4	28	41.2	21	30	26.5	13	36	27.5	11	29			
chr6	4049040	T	G	0.0	0	58	13.0	7	47	0.0	0	28	0.0	0	45	2.0	1	48	7.5	3	37			
chr6	41939978	A	G	68.4	26	12	56.4	22	17	65.4	17	9	0	18	0	21.3	10	37	37.1	13	22			
chr6	57813373	G	T	2.0	1	50	13.6	6	38	0.0	0	31	0.0	0	30	1.9	1	53	0.0	0	28			
chr6	58140874	A	G	0.0	0	33	4.9	2	39	0.0	0	15	0.0	0	18	3.4	1	28	26.1	6	17			
chr6	66221259	T	A	10.7	3	25	10.3	4	35	55.2	16	13	50.0	14	14	0.0	0	34	13.5	5	32			
chr6	86676221	G	A	6.5	2	29	27.9	12	31	18.2	6	27	8.0	2	23	17.1	7	34	7.1	2	26			
chr6	99741570	G	C	0.0	0	52	9.6	5	47	0.0	0	30	0.0	0	33	0.0	0	32	0.0	0	36			
chr7	104138450	T	G	0.0	0	37	4.8	3	59	0.0	0	43	0.0	0	45	14.8	8	46	22.7	10	34			
chr7	104255123	C	T	0.0	0	48	10.9	5	41	0.0	0	22	0.0	0	39	0.0	0	34	0.0	0	38			
chr7	106087606	A	G	0.0	0	27	0.0	0	37	6.7	2	28	13.3	4	26	0.0	0	48	0.0	0	36			
chr7	116163157	G	A	0.0	0	16	7.1	1	13	0.0	0	21	0.0	0	20	0.0	0	29	13.6	3	19			
chr7	116495867	T	C	4.5	2	42	4.8	2	40	0.0	0	25	19.4	6	25	4.5	2	42	2.3	1	43			
chr7	138029031	A	G	1.6	1	60	13.2	9	59	0.0	0	41	0.0	0	44	21.3	19	70	18.6	11	48			
chr7	141679331	G	C	0.0	0	49	9.6	5	47	18.2	4	18	3.4	1	28	0.0	0	45	2.6	1	37			
chr7	142111761	A	T	8.5	6	65	15.1	13	73	0.0	0	31	22.9	8	27	10.4	7	60	2.3	1	42			
chr7	142111913	A	G	9.6	7	66	8.0	7	80	4.0	1	24	15.4	4	22	0.0	0	50	10.6	5	42			
chr7	142148845	A	G	18.9	10	43	21.8	12	43	0.0	0	32	20.5	9	35	15.6	7	38	17.9	7	32			
chr7	142148846	C	A	18.9	10	43	22.4	13	45	0.0	0	32	20.5	9	35	15.2	7	39	17.9	7	32			
chr7	142148850	G	A	18.9	10	43	19.3	11	46	0.0	0	31	20.0	9	36	16.3	7	36	22.0	9	32			
chr7	142166768	A	G	5.7	4	66	7.3	6	76	6.5	2	29	3.3	1	29	0.0	0	59	11.1	4	32			
chr7	142473180	G	A	1.5	1	65	8.0	8	92	7.7	2	24	8.1	3	34	0.0	0	56	0.0	0	39			
chr7	14399404	T	A	6.8	3	41	3.8	2	51	0.0	0	26	12.9	4	27	2.3	1	43	5.6	2	34			
chr7	14399408	A	C	7.0	3	40	3.8	2	50	0.0	0	25	13.3	4	26	2.3	1	42	2.9	1	34			
chr7	149732086	T	C	4.3	3	67	1.6	1	63	3.2	1	30	28.9	11	27	25.6	10	29	4.3	1	22			
chr7	151068449	A	C	14.3	5	30	34.3	12	23	40.0	8	12	21.1	4	15	21.1	8	30	10.3	3	26			
chr7	151934369	G	A	6.3	11	163	6.0	10	158	2.9	3	99	11.2	14	111	12.9	23	155	4.5	6	128			
chr7	151934376	T	G	4.1	7	163	6.7	11	154	3.0	3	98	8.9	11	113	11.6	20	152	3.1	4	126			
chr7	151938099	G	T	1.7	1	57	4.8	3	60	0.0	0	39	5.7	2	33	0.0	0	48	18.8	6	26			
chr7	151938897	G	A	0.0	0	39	0.0	0	42	0.0	0	26	16.7	5	25	17.5	7	33	7.0	3	40			
chr7	151983234	C	A	2.2	3	136	9.7	14	130	0.7	1	138	6.8	9	124	5.4	10	175	8.1	12	136			
chr7	152084879	T	C	2.9	1	34	0.0	0	31	0.0	0	42	30.0	12	28	13.8	8	50	26.3	10	28			
chr7	152087886	G	A	0.0	0	43	0.0	0	48	2.2	1	45	7.9	3	35	0.0	0	51	12.8	6	41			

				Subject 1							Subject 2							Subject 3							
chr7	152087958	G	A	2.0	1	50	0.0	0	48	10.7	3	25	11.8	4	30	0.0	0	43	15.4	6	33				
chr7	152087961	A	G	2.0	1	49	2.0	1	48	9.4	3	29	11.4	4	31	0.0	0	45	17.1	7	34				
chr7	153451236	C	T	0.0	0	43	0.0	0	36	0.0	0	46	21.4	12	44	0.0	0	52	0.0	0	37				
chr7	155862144	T	C	0.0	0	55	0.0	0	57	3.8	1	25	24.4	10	31	34.6	9	17	42.5	17	23				
chr7	155862148	C	T	0.0	0	54	0.0	0	57	4.0	1	24	24.4	10	31	0.0	0	25	0.0	0	42				
chr7	157787678	G	T	0.0	0	35	13.9	5	31	0.0	0	3	0.0	0	8	16.7	1	5	0.0	0	4				
chr7	158126544	A	G	3.9	3	73	7.7	5	60	5.3	2	36	6.1	3	46	7.4	4	50	2.7	1	36				
chr7	158598790	G	A	21.1	8	30	30.8	8	18	0.0	0	30	23.7	9	29	8.2	4	45	12.1	4	29				
chr7	158598839	C	T	21.6	11	40	27.0	10	27	0.0	0	37	24.0	12	38	11.9	8	59	10.6	5	42				
chr7	158598842	A	G	39.3	22	34	38.5	15	24	0.0	0	37	25.0	13	39	11.9	8	59	12.5	6	42				
chr7	17665369	A	G	27.5	11	29	34.2	13	25	0.0	0	21	32.0	8	17	31.6	12	26	22.2	6	21				
chr7	1943625	T	C	0.0	0	53	13.0	7	47	0.0	0	20	12.5	2	14	0.0	0	44	0.0	0	30				
chr7	31751896	G	A	15.0	9	51	17.9	15	69	33.3	11	22	13.0	6	40	31.6	18	39	20.0	9	36				
chr7	38236734	C	T	4.9	3	58	10.2	5	44	14.3	6	36	3.1	1	31	7.3	4	51	18.6	8	35				
chr7	38236737	T	C	40.7	24	35	45.8	22	26	16.7	7	35	3.1	1	31	7.4	4	50	16.7	7	35				
chr7	38293238	C	A	5.1	2	37	8.5	4	43	0.0	0	33	0.0	0	48	6.1	2	31	0.0	0	28				
chr7	397199	G	A	10.2	26	230	9.0	22	222	4.7	3	61	9.3	8	78	7.9	5	58	5.7	3	50				
chr7	39903821	A	T	0.0	0	27	0.0	0	26	0.0	0	47	0.0	0	29	0.0	0	53	10.5	4	34				
chr7	47402749	T	C	0.7	1	149	2.2	3	134	2.6	1	38	5.9	2	32	1.6	1	60	16.2	6	31				
chr7	48165761	C	T	0.0	0	39	0.0	0	41	20.6	7	27	35.9	14	25	0.0	0	51	0.0	0	41				
chr7	48894320	G	C	3.9	2	49	2.0	1	50	3.2	1	30	10.0	4	36	0.0	0	50	10.3	4	35				
chr7	48894362	T	G	4.5	2	42	2.9	2	66	3.1	1	31	10.3	4	35	0.0	0	55	10.8	4	33				
chr7	49307012	A	T	6.7	1	14	9.7	3	28	28.6	10	25	45.8	11	13	0.0	0	29	33.3	13	26				
chr7	5314972	G	A	5.1	4	75	9.7	7	65	7.1	3	39	19.6	10	41	10.4	5	43	7.1	3	39				
chr7	53222321	C	G	5.3	2	36	9.1	3	30	0.0	0	31	11.8	4	30	9.3	4	39	5.3	2	36				
chr7	53222359	T	C	6.3	2	30	30.8	12	27	7.0	3	40	17.6	6	28	11.9	5	37	13.6	6	38				
chr7	53222377	G	T	0.0	0	36	7.7	3	36	0.0	0	45	10.3	4	35	6.3	3	45	5.9	3	48				
chr7	53222454	T	G	6.5	2	29	0.0	0	28	0.0	0	43	8.8	3	31	0.0	0	45	3.0	2	64				
chr7	53225520	A	G	17.7	14	65	6.5	5	72	4.3	2	44	16.7	7	35	14.7	11	64	9.3	5	49				
chr7	53226000	C	A	18.6	8	35	10.6	5	42	0.0	0	31	14.8	4	23	6.3	4	60	11.9	5	37				
chr7	53230619	T	C	19.0	12	51	21.4	15	55	0.0	0	32	23.8	10	32	6.1	4	62	21.2	11	41				
chr7	53232089	G	A	0.0	0	38	11.4	4	31	7.3	3	38	5.1	2	37	6.0	3	47	8.9	4	41				
chr7	56185948	G	A	0.0	0	33	0.0	0	41	7.9	3	35	8.3	3	33	2.1	1	46	29.3	12	29				
chr7	56927376	T	C	7.4	2	25	7.9	3	35	6.7	2	28	19.4	6	25	9.5	4	38	3.4	1	28				
chr7	57610585	C	G	0.0	0	144	0.0	0	138	0.0	0	60	6.4	5	73	4.6	4	83	5.6	5	85				
chr7	57611713	T	A	11.1	10	80	10.6	10	84	0.0	0	47	10.0	7	63	7.0	7	93	9.7	10	93				
chr7	57612466	A	G	5.5	3	52	7.7	3	36	5.6	2	34	9.5	4	38	0.0	0	61	10.0	6	54				
chr7	57634401	A	G	0.0	0	81	0.0	0	83	0.0	0	61	0.0	0	70	0.0	0	95	4.8	4	80				
chr7	57730945	T	C	15.4	8	44	14.3	9	54	0.0	0	51	14.3	9	54	8.5	5	54	9.3	5	49				
chr7	57730953	G	T	13.2	7	46	12.5	8	56	0.0	0	53	16.2	11	57	11.6	8	61	8.9	5	51				
chr7	57732835	G	T	14.5	10	59	12.2	9	65	3.8	2	50	8.2	4	45	4.4	3	65	16.9	10	49				
chr7	57732845	G	A	12.9	9	61	10.3	8	70	3.6	2	54	8.2	4	45	2.8	2	70	19.3	11	46				
chr7	57732856	G	T	13.7	10	63	10.4	8	69	7.1	4	52	8.3	4	44	2.8	2	69	16.4	10	51				
chr7	57733654	C	T	3.6	3	80	1.8	1	56	4.9	2	39	2.0	1	50	0.0	0	84	7.2	5	64				
chr7	57745988	T	C	2.3	2	86	11.9	12	89	13.5	10	64	10.8	7	58	9.6	11	103	8.9	8	82				
chr7	57745990	C	A	2.3	2	85	13.0	13	87	13.3	10	65	9.2	6	59	9.6	11	104	7.7	7	84				
chr7	57747838	G	A	1.5	1	64	9.1	7	70	12.0	6	44	12.5	11	77	10.0	9	81	6.9	7	94				

				Subject 1							Subject 2							Subject 3						
chr7	57747864	T	C	1.5	1	67	8.4	7	76	12.3	7	50	14.5	11	65	9.2	9	89	7.9	8	93			
chr7	57747882	G	T	7.2	5	64	11.7	9	68	21.3	10	37	18.3	13	58	9.9	9	82	8.1	8	91			
chr7	57759655	G	C	0.0	0	24	15.0	3	17	0.0	0	46	10.3	3	26	7.5	3	37	2.6	1	37			
chr7	57773386	G	C	1.8	1	55	10.8	7	58	9.1	4	40	12.5	7	49	15.1	16	90	10.1	8	71			
chr7	57780232	T	C	0.0	0	40	3.2	1	30	7.5	3	37	4.9	2	39	0.0	0	53	9.1	4	40			
chr7	57790346	G	A	1.3	1	79	5.6	5	85	2.6	1	37	11.1	6	48	10.5	6	51	9.4	5	48			
chr7	57815280	A	C	0.0	0	34	0.0	0	33	0.0	0	38	8.7	4	42	9.3	4	39	8.1	3	34			
chr7	57826640	G	A	0.0	0	52	10.9	5	41	12.7	7	48	5.0	2	38	0.0	0	56	0.0	0	44			
chr7	57826648	C	T	0.0	0	45	10.9	5	41	13.7	7	44	2.6	1	38	0.0	0	63	0.0	0	41			
chr7	57847045	T	G	5.1	2	37	7.7	3	36	0.0	0	34	9.1	4	40	6.3	3	45	7.3	4	51			
chr7	57866585	G	A	14.8	8	46	7.1	4	52	0.0	0	39	14.3	4	24	3.9	2	49	13.3	4	26			
chr7	57916985	G	A	7.1	6	79	3.8	3	77	3.6	4	108	6.7	8	112	2.9	4	135	8.8	10	103			
chr7	57922532	A	C	2.2	2	90	3.4	3	85	1.0	1	98	5.5	5	86	7.3	8	101	4.9	5	98			
chr7	57924351	T	C	2.4	1	41	25.0	11	33	29.8	17	40	16.4	9	46	25.8	17	49	22.2	12	42			
chr7	57937835	G	A	20.0	8	32	18.6	8	35	0.0	0	27	15.8	6	32	3.0	1	32	5.1	2	37			
chr7	61071494	A	G	3.8	2	51	15.4	8	44	20.7	6	23	21.2	7	26	3.4	2	56	9.3	5	49			
chr7	61077447	T	C	2.3	3	125	3.2	5	153	1.9	2	105	6.3	7	104	0.0	0	145	0.0	0	110			
chr7	61077451	A	C	3.8	5	125	4.2	7	158	1.8	2	112	7.2	8	103	2.1	3	141	2.7	3	109			
chr7	61738853	A	C	7.7	16	192	3.3	7	204	0.7	1	141	10.1	15	133	2.8	5	175	1.2	2	167			
chr7	61739271	G	A	0.0	0	89	7.4	10	125	4.6	7	145	5.4	6	106	2.7	5	182	5.7	7	116			
chr7	61770506	T	C	6.9	2	27	8.8	3	31	2.6	1	38	0.0	0	34	0.0	0	41	17.1	6	29			
chr7	61784409	A	G	7.5	22	272	8.1	28	317	15.4	30	165	17.9	45	206	3.0	8	261	9.0	21	213			
chr7	61803552	T	C	0.0	0	202	3.1	7	216	1.0	2	198	1.4	3	212	2.7	7	248	3.6	8	216			
chr7	61804008	C	G	3.1	5	156	2.6	4	147	0.8	1	126	4.8	5	99	1.5	2	131	5.7	7	116			
chr7	61804083	A	G	0.6	1	175	2.9	5	168	0.8	1	131	5.5	7	120	5.1	8	150	2.1	3	141			
chr7	61804113	T	C	1.4	2	141	2.6	4	150	0.8	1	125	5.4	7	123	9.5	14	134	1.4	2	140			
chr7	61825966	C	G	0.8	1	122	6.3	8	120	7.8	6	71	10.3	9	78	5.5	6	103	2.1	2	94			
chr7	61826012	G	T	0.0	0	200	1.1	2	186	1.3	1	74	0.9	1	110	0.8	1	123	6.3	7	104			
chr7	61832107	A	T	4.5	2	42	1.8	1	54	1.0	1	97	6.3	5	74	6.5	7	100	4.2	4	91			
chr7	63280418	T	C	22.7	10	34	12.5	7	49	23.3	10	33	17.6	9	42	2.1	1	47	9.8	4	37			
chr7	64959114	G	T	0.0	0	44	15.2	5	28	16.0	8	42	16.3	7	36	11.1	4	32	8.5	4	43			
chr7	64960937	G	C	0.0	0	47	0.0	0	67	6.7	5	70	4.8	3	60	0.0	0	78	10.7	8	67			
chr7	64965192	A	G	2.6	1	38	0.0	0	67	2.4	1	40	8.8	3	31	0.0	0	48	12.5	6	42			
chr7	64965198	A	T	0.0	0	31	0.0	0	63	2.3	1	42	15.6	5	27	0.0	0	43	11.4	5	39			
chr7	65086473	T	C	5.6	2	34	2.6	1	37	0.0	0	21	3.8	1	25	0.0	0	47	8.5	4	43			
chr7	65086484	A	G	6.3	2	30	2.6	1	38	0.0	0	23	0.0	0	23	0.0	0	47	8.9	4	41			
chr7	67605748	G	C	0.0	0	45	9.1	5	50	0.0	0	35	0.0	0	53	1.9	1	51	4.1	2	47			
chr7	72158179	A	G	0.0	0	50	0.0	0	51	0.0	0	20	0.0	0	44	0.0	0	41	16.7	8	40			
chr7	75717965	C	T	0.0	0	45	20.0	7	28	10.5	2	17	0.0	0	18	22.7	5	17	15.8	3	16			
chr7	76679530	A	T	0.0	0	45	14.7	5	29	20.6	7	27	2.6	1	37	0.0	0	46	0.0	0	35			
chr7	76739080	A	T	0.0	0	38	0.0	0	37	0.0	0	54	10.3	4	35	5.3	2	36	6.7	2	28			
chr7	78585106	A	T	3.1	1	31	8.6	3	32	2.9	1	34	21.4	9	33	2.6	1	38	3.1	1	31			
chr7	8604401	C	A	0.0	0	40	10.9	6	49	0.0	0	37	0.0	0	35	0.0	0	58	0.0	0	47			
chr7	97554471	A	G	22.2	10	35	30.6	11	25	0.0	0	17	21.4	6	22	6.7	2	28	9.1	2	20			
chr7	98875543	A	T	20.4	11	43	22.2	14	49	0.0	0	21	3.1	1	31	22.0	9	32	20.8	5	19			
chr7	99782384	T	C	16.7	8	40	8.1	3	34	0.0	0	28	15.2	5	28	13.2	7	46	3.1	1	31			
chr8	104769207	C	G	22.6	7	24	34.8	8	15	3.6	1	27	18.9	7	30	29.2	7	17	31.3	10	22			

				Subject 1					Subject 2					Subject 3							
chr8	109110445	G	A	0.0	0	56	8.5	5	54	0.0	0	36	0.0	0	41	1.7	1	59	0.0	0	28
chr8	111740618	C	T	0.0	0	34	0.0	0	40	0.0	0	27	0.0	0	29	0.0	0	43	14.7	5	29
chr8	115126910	G	A	25.9	7	20	42.1	16	22	36.4	16	28	9.4	3	29	26.9	18	49	20.0	8	32
chr8	115379427	A	G	8.3	3	33	8.6	5	53	5.9	2	32	25.0	9	27	0.0	0	38	0.0	0	44
chr8	12426498	A	G	0.0	0	166	0.0	0	159	0.0	0	103	4.4	6	129	0.0	0	101	0.0	0	92
chr8	12426504	A	G	0.0	0	164	0.0	0	156	0.0	0	102	4.4	6	129	0.0	0	99	0.0	0	95
chr8	1266302	G	A	0.0	0	35	17.8	8	37	0.0	0	15	4.0	1	24	12.5	3	21	14.3	3	18
chr8	1266308	G	T	2.7	1	36	17.4	8	38	0.0	0	17	0.0	0	25	7.7	2	24	12.5	3	21
chr8	132364257	G	T	29.8	17	40	11.4	8	62	0.0	0	37	0.0	0	46	33.3	20	40	33.9	20	39
chr8	1333276	C	T	0.0	0	98	5.8	4	65	0.0	0	16	0.0	0	18	9.1	2	20	0.0	0	34
chr8	138873822	A	G	15.2	5	28	23.8	10	32	20.0	5	20	25.0	7	21	0.0	0	23	0.0	0	48
chr8	142083612	A	T	6.0	4	63	11.7	9	68	23.5	8	26	27.1	13	35	14.6	6	35	21.2	11	41
chr8	143183616	G	A	0.6	1	154	0.0	0	130	0.0	0	26	19.2	5	21	9.5	6	57	4.8	2	40
chr8	144287321	C	A	0.0	0	28	12.8	6	41	0.0	0	16	0.0	0	21	0.0	0	23	0.0	0	21
chr8	144472772	A	C	2.3	2	86	3.1	3	94	2.9	1	33	14.3	7	42	9.1	4	40	3.2	1	30
chr8	43837209	T	A	3.4	8	226	2.2	5	221	0.8	1	130	4.9	7	136	0.0	0	148	0.0	0	120
chr8	43837729	C	A	2.7	6	214	2.1	4	186	0.6	1	169	4.7	8	162	1.1	4	349	0.9	2	229
chr8	46843436	A	C	0.0	0	130	0.0	0	156	1.6	2	122	4.5	9	190	1.8	8	425	1.6	6	359
chr8	48546152	T	G	14.5	8	47	30.6	19	43	30.2	13	30	29.2	14	34	15.3	9	50	22.7	10	34
chr8	66068264	G	T	4.5	2	42	11.8	6	45	47.1	16	18	60.0	18	12	0.0	0	35	0.0	0	43
chr8	74993223	T	C	0.0	0	52	0.0	0	65	4.5	1	21	14.6	7	41	52.4	11	10	58.1	18	13
chr8	79813739	G	C	29.6	16	38	21.4	12	44	13.0	3	20	31.8	14	30	26.5	13	36	44.1	15	19
chr8	87545298	T	A	20.6	7	27	18.2	8	36	0.0	0	27	0.0	0	40	3.1	1	31	25.6	11	32
chr8	88642185	G	A	0.0	0	28	0.0	0	19	33.3	6	12	18.2	4	18	0.0	0	20	44.4	8	10
chr9	108214996	C	T	3.3	1	29	0.0	0	25	0.0	0	20	0.0	0	24	2.9	1	33	13.3	4	26
chr9	117177564	A	C	14.5	8	47	15.4	10	55	0.0	0	28	0.0	0	34	0.0	0	45	0.0	0	41
chr9	121688934	T	A	0.0	0	40	0.0	0	37	0.0	0	29	0.0	0	30	0.0	0	25	22.6	7	24
chr9	121846699	T	C	0.0	0	28	0.0	0	46	0.0	0	31	2.7	1	36	0.0	0	37	13.5	5	32
chr9	121973486	A	T	0.0	0	19	15.8	3	16	0.0	0	19	20.7	6	23	0.0	0	40	0.0	0	24
chr9	12365179	G	C	29.2	14	34	39.6	21	32	26.3	10	28	32.6	14	29	31.7	19	41	41.3	19	27
chr9	124774959	A	G	2.7	1	36	11.8	4	30	4.2	1	23	3.7	1	26	0.0	0	49	9.7	3	28
chr9	128492353	G	A	18.6	8	35	12.5	5	35	5.9	2	32	13.7	7	44	7.0	3	40	5.4	2	35
chr9	132154844	C	A	0.0	0	36	0.0	0	37	0.0	0	30	11.1	4	32	0.0	0	37	0.0	0	37
chr9	137639822	C	T	0.0	0	164	0.0	0	149	0.0	0	22	0.0	0	29	4.7	2	41	21.9	7	25
chr9	140675307	A	G	14.0	14	86	14.0	12	74	4.5	1	21	3.8	1	25	0.0	0	32	18.8	6	26
chr9	141037486	G	A	0.0	0	103	0.0	0	89	0.0	0	24	20.8	5	19	4.9	2	39	3.3	1	29
chr9	141067308	C	T	4.5	5	105	6.4	7	103	1.4	1	68	8.5	7	75	7.3	10	127	5.2	4	73
chr9	141083491	G	T	9.5	2	19	9.7	3	28	2.7	1	36	6.0	3	47	0.0	0	42	30.8	8	18
chr9	20649315	A	G	0.0	0	33	0.0	0	22	5.3	1	18	29.0	9	22	0.0	0	45	0.0	0	34
chr9	33390969	C	T	0.0	0	23	28.6	6	15	17.6	3	14	33.3	7	14	25.0	4	12	5.9	1	16
chr9	33793265	C	G	0.0	0	49	10.7	6	50	5.7	2	33	16.7	6	30	0.0	0	61	0.0	0	51
chr9	35879881	C	T	9.5	2	19	26.5	9	25	0.0	0	37	0.0	0	24	7.9	3	35	36.0	9	16
chr9	37816660	T	G	14.3	4	24	24.1	7	22	0.0	0	33	0.0	0	27	1.9	1	51	0.0	0	33
chr9	38538810	G	A	2.9	1	34	0.0	0	24	8.0	2	23	7.1	1	13	0.0	0	34	16.7	4	20
chr9	43562969	A	T	0.0	0	86	1.3	1	79	1.8	1	54	1.6	1	60	0.0	0	67	6.5	6	87
chr9	44828734	T	C	7.1	2	26	5.9	2	32	0.0	0	14	23.1	6	20	0.0	0	30	20.8	5	19
chr9	44828773	C	T	6.1	2	31	12.5	4	28	0.0	0	19	23.1	6	20	0.0	0	32	20.0	5	20

				Subject 1							Subject 2							Subject 3							
chr9	44899366	A	C	3.3	1	29	7.5	3	37	0.0	0	40	23.5	8	26	6.8	5	68	9.3	4	39				
chr9	44899502	C	T	17.1	7	34	15.0	6	34	0.0	0	38	16.1	9	47	0.0	0	61	11.4	5	39				
chr9	44899511	C	T	17.8	8	37	15.4	6	33	0.0	0	41	16.7	9	45	0.0	0	66	11.4	5	39				
chr9	44899576	T	A	14.6	6	35	2.7	1	36	0.0	0	43	8.0	4	46	4.9	3	58	10.3	4	35				
chr9	44902021	G	A	7.0	3	40	2.3	1	43	6.7	2	28	2.6	1	37	0.0	0	48	14.3	5	30				
chr9	45054947	G	A	2.6	1	38	14.3	6	36	2.8	1	35	6.1	2	31	14.3	6	36	11.9	5	37				
chr9	66471785	A	G	1.6	4	245	1.8	4	219	1.6	2	120	8.3	14	154	6.9	16	216	9.6	21	197				
chr9	66478775	A	G	0.7	1	149	0.0	0	168	1.2	1	81	4.8	5	99	0.0	0	139	0.0	0	119				
chr9	66486725	C	T	1.8	3	168	6.7	12	167	5.2	6	109	1.9	2	101	1.4	2	146	4.3	5	111				
chr9	66497909	G	A	0.0	0	153	0.0	0	146	0.6	1	155	5.8	9	146	4.6	10	206	2.1	3	138				
chr9	66507005	C	T	1.2	1	81	1.1	1	86	0.0	0	68	6.2	5	76	7.7	7	84	7.8	6	71				
chr9	66515394	T	G	10.9	5	41	1.5	1	67	3.0	2	65	1.8	1	56	0.0	0	63	7.0	4	53				
chr9	66710555	T	C	0.0	0	39	9.1	5	50	9.0	7	71	9.8	5	46	16.7	9	45	11.9	8	59				
chr9	68280026	C	T	5.0	1	19	20.7	6	23	0.0	0	30	13.2	5	33	7.4	4	50	2.9	1	34				
chr9	68318416	T	G	3.7	3	79	9.3	7	68	19.1	9	38	7.4	4	50	2.4	2	80	4.2	2	46				
chr9	68353820	A	T	5.1	4	75	1.3	1	77	3.7	3	78	1.4	1	68	1.0	1	103	9.3	7	68				
chr9	68357366	A	G	13.2	19	125	25.9	38	109	0.0	0	75	11.6	13	99	7.6	10	121	8.3	10	110				
chr9	68378970	G	A	11.6	5	38	18.2	6	27	2.9	1	33	7.5	3	37	0.0	0	45	7.1	4	52				
chr9	68378978	T	C	7.1	3	39	18.2	6	27	2.6	1	37	8.2	4	45	1.9	1	52	8.1	5	57				
chr9	68388344	T	C	0.0	0	195	2.3	5	208	1.0	1	101	1.8	2	107	0.6	1	162	3.4	5	144				
chr9	68389967	G	A	4.1	6	139	7.3	13	166	4.2	5	115	5.3	7	125	4.4	8	174	10.4	17	147				
chr9	68397934	A	G	5.2	6	110	17.6	26	122	16.4	30	153	12.1	21	152	16.0	26	137	9.5	19	182				
chr9	68404574	T	A	3.0	2	64	2.1	2	93	4.3	4	88	3.3	4	117	1.2	2	167	4.3	6	134				
chr9	68406743	G	A	2.8	3	106	4.5	6	128	1.6	2	127	7.1	9	118	4.9	10	193	6.9	10	134				
chr9	68435125	C	T	7.0	6	80	7.6	7	85	1.2	1	85	6.3	5	75	6.7	7	98	1.3	1	79				
chr9	68436204	A	C	4.3	5	111	3.9	5	122	1.0	1	98	8.5	10	107	1.8	3	162	3.0	3	98				
chr9	68446485	A	G	0.0	0	39	3.7	1	26	6.5	2	29	20.0	4	16	5.7	2	33	10.9	5	41				
chr9	68450412	C	A	0.0	0	120	1.4	2	138	1.7	1	57	6.3	6	89	2.4	3	122	3.7	4	105				
chr9	68450751	C	T	4.8	4	80	3.7	4	104	0.0	0	95	9.2	8	79	8.8	12	125	21.2	22	82				
chr9	68469564	A	G	6.6	11	156	5.4	10	176	0.0	0	115	2.3	3	127	0.5	1	183	4.3	7	155				
chr9	68474683	G	C	2.8	3	105	2.3	3	125	3.1	4	127	6.3	8	120	2.0	4	196	5.2	10	184				
chr9	68476047	T	G	1.8	1	56	1.4	1	72	7.8	4	47	13.6	6	38	5.4	3	53	15.3	9	50				
chr9	68481746	C	T	5.9	5	80	3.8	3	75	2.0	1	48	2.8	2	70	0.0	0	88	8.3	8	88				
chr9	68486828	C	A	3.6	2	53	4.0	2	48	0.0	0	44	14.6	7	41	10.3	6	52	10.8	8	66				
chr9	68508813	T	C	1.7	3	170	7.5	14	172	8.3	12	132	8.8	12	125	12.3	24	171	7.8	12	142				
chr9	68675353	C	A	2.1	1	47	6.8	3	41	0.0	0	51	7.8	4	47	0.0	0	75	3.2	2	61				
chr9	68675830	G	A	0.0	0	17	0.0	0	16	0.0	0	15	0.0	0	27	0.0	0	51	16.1	5	26				
chr9	68689069	G	T	3.4	10	283	1.6	5	302	0.0	0	94	0.0	0	140	1.5	3	196	6.5	14	200				
chr9	68698783	T	C	0.9	1	109	6.6	8	113	1.5	1	65	3.4	2	57	0.0	0	107	1.5	1	67				
chr9	68698809	G	T	0.0	0	49	9.7	6	56	5.6	3	51	7.9	3	35	3.7	3	78	5.8	3	49				
chr9	68703256	T	C	6.6	6	85	11.7	12	91	9.7	7	65	7.5	7	86	14.0	20	123	14.9	13	74				
chr9	68721863	C	A	1.4	1	71	7.9	6	70	3.2	2	61	3.4	2	57	2.2	2	89	3.0	2	65				
chr9	68744741	T	C	3.4	5	141	3.6	5	135	1.9	2	106	2.2	2	91	0.0	0	108	5.6	5	85				
chr9	68996791	C	T	1.9	2	103	1.0	1	101	0.0	0	64	11.1	9	72	0.0	0	75	1.2	1	80				
chr9	69021023	C	T	2.4	2	81	5.7	7	115	1.6	1	63	7.0	5	66	4.2	4	92	3.2	3	90				
chr9	69034059	G	A	0.0	0	135	6.4	9	131	0.0	0	119	0.0	0	127	3.8	7	179	3.5	5	136				
chr9	69059558	T	C	9.5	7	67	3.0	2	64	1.5	1	67	1.4	1	71	2.2	2	89	8.1	7	79				

				Subject 1						Subject 2						Subject 3					
				17.4	12	57	19.5	15	62	5.7	2	33	5.6	3	51	7.3	4	51	22.2	12	42
chr9	69073389	A	G	17.4	12	57	19.5	15	62	5.7	2	33	5.6	3	51	7.3	4	51	22.2	12	42
chr9	69075239	A	G	5.1	7	130	1.5	2	134	0.0	0	185	0.0	0	151	0.5	1	204	4.6	8	167
chr9	69415557	A	G	0.0	0	44	22.9	8	27	0.0	0	23	9.1	3	30	25.0	9	27	28.6	8	20
chr9	69839232	C	T	0.0	0	65	0.0	0	60	0.0	0	50	8.6	5	53	19.1	13	55	11.5	6	46
chr9	70632435	T	C	13.8	4	25	7.7	1	12	5.6	1	17	0.0	0	21	0.0	0	28	21.2	7	26
chr9	70667777	G	A	0.0	0	54	6.2	4	61	0.0	0	31	0.0	0	29	10.7	6	50	0.0	0	40
chr9	70667804	A	C	0.0	0	73	9.3	7	68	0.0	0	32	0.0	0	19	6.8	6	82	2.1	1	47
chr9	78790241	T	C	3.3	2	58	6.8	4	55	7.9	3	35	9.7	3	28	1.7	1	59	15.6	5	27
chr9	80412493	C	T	0.0	0	58	12.3	9	64	0.0	0	28	3.7	2	52	0.0	0	48	2.6	1	38
chr9	84406460	T	C	0.0	0	24	26.7	8	22	25.7	9	26	32.6	14	29	4.8	2	40	6.7	2	28
chr9	84406461	C	T	0.0	0	24	26.7	8	22	28.6	10	25	41.5	17	24	7.0	3	40	10.0	3	27
chr9	89058025	C	T	34.3	12	23	59.3	35	24	19.0	4	17	44.0	11	14	18.8	3	13	22.6	7	24
chr9	93508645	T	C	1.3	1	74	2.8	2	70	0.0	0	38	11.1	4	32	5.7	3	50	2.2	1	44
chr9	97650615	A	G	31.6	12	26	44.2	19	24	17.9	5	23	34.5	10	19	38.5	25	40	40.0	14	21
chr9	99906109	C	A	0.0	0	63	1.8	1	55	0.0	0	39	9.3	4	39	0.0	0	48	2.0	1	48
chr9	99933073	A	C	0.0	0	14	3.6	1	27	0.0	0	39	17.4	4	19	5.4	2	35	5.7	2	33
chr10	102777652	A	G	12.8	6	41	8.6	5	53	12.5	3	21	20.8	5	19	15.8	6	32	21.3	10	37
chr10	102856	A	G	0.0	0	30	0.0	0	41	11.8	4	30	0.0	0	41	0.0	0	41	9.4	5	48
chr10	107915497	A	T	23.1	9	30	34.1	15	29	30.3	10	23	44.4	16	20	32.0	16	34	37.0	10	17
chr10	1091823	G	A	13.2	7	46	14.3	8	48	13.3	4	26	24.4	11	34	25.0	14	42	22.9	11	37
chr10	109597	T	G	2.6	1	38	2.2	1	44	0.0	0	38	12.9	4	27	4.3	2	45	6.1	2	31
chr10	126218382	G	A	21.2	21	78	34.0	32	62	28.0	7	18	35.1	13	24	27.7	13	34	26.1	12	34
chr10	127602862	T	A	17.0	8	39	27.0	17	46	44.9	111	136	41.3	88	125	34.1	91	176	40.5	92	135
chr10	130381617	A	C	5.0	2	38	10.8	4	33	0.0	0	21	11.1	2	16	0.0	0	39	10.5	4	34
chr10	134249647	C	T	0.0	0	53	0.0	0	49	4.5	1	21	32.1	9	19	0.0	0	73	1.8	1	55
chr10	135467779	G	T	0.0	0	39	12.8	6	41	0.0	0	28	0.0	0	44	16.0	4	21	2.9	1	33
chr10	135468482	G	T	0.0	0	87	0.0	0	87	0.0	0	53	10.6	7	59	3.8	3	75	4.3	3	67
chr10	17516827	T	G	0.0	0	36	13.0	6	40	0.0	0	26	0.0	0	39	0.0	0	42	2.4	1	40
chr10	21516582	T	C	0.0	0	48	0.0	0	65	0.0	0	40	8.9	4	41	3.8	2	50	2.0	1	48
chr10	26917730	A	G	6.9	2	27	17.0	8	39	0.0	0	37	13.2	5	33	14.1	9	55	27.3	12	32
chr10	28840749	T	G	25.8	8	23	25.9	7	20	8.3	1	11	28.1	9	23	5.3	2	36	29.4	10	24
chr10	29623341	T	C	56.5	13	10	41.2	7	10	24.1	7	22	40.0	8	12	46.7	14	16	30.4	7	16
chr10	3019743	G	A	16.7	4	20	9.5	2	19	5.9	1	16	46.2	6	7	4.5	1	21	0.0	0	16
chr10	30968291	C	A	11.3	6	47	9.1	3	30	3.7	1	26	21.9	7	25	2.4	1	41	11.1	5	40
chr10	32122263	A	T	10.9	6	49	21.3	10	37	0.0	0	35	0.0	0	42	6.3	3	45	12.5	5	35
chr10	35111730	A	T	0.0	0	29	19.4	7	29	0.0	0	25	19.4	6	25	3.6	2	53	13.0	3	20
chr10	36118405	C	T	0.0	0	24	0.0	0	20	12.5	3	21	29.4	5	12	0.0	0	27	15.6	5	27
chr10	36118407	T	C	0.0	0	24	0.0	0	20	12.5	3	21	29.4	5	12	0.0	0	28	12.9	4	27
chr10	38909247	A	G	8.3	3	33	3.0	1	32	9.1	2	20	5.0	1	19	0.0	0	30	27.3	6	16
chr10	38964254	A	G	5.9	1	16	5.0	1	19	0.0	0	33	18.5	5	22	5.3	2	36	20.0	5	20
chr10	42612222	C	T	6.3	4	59	14.4	14	83	6.9	4	54	14.9	7	40	15.8	12	64	19.2	14	59
chr10	42648403	G	C	7.0	10	132	9.4	13	126	5.7	6	99	5.3	5	89	1.6	2	126	6.8	9	123
chr10	42650568	C	T	2.2	6	262	2.7	8	287	1.7	2	119	6.8	10	138	2.7	6	216	5.8	9	145
chr10	42656645	A	T	7.1	6	79	3.6	3	80	3.9	3	73	6.3	5	74	8.0	11	126	12.6	16	111
chr10	42656648	T	A	7.1	6	78	2.4	2	80	2.7	2	72	5.9	5	80	5.2	7	127	11.3	14	110
chr10	42656973	C	G	2.6	3	112	9.0	9	91	0.0	0	68	5.3	4	72	2.0	2	99	4.0	4	95
chr10	42724718	T	A	0.0	0	24	0.0	0	34	12.9	4	27	14.6	6	35	0.0	0	45	11.6	5	38

				Subject 1							Subject 2							Subject 3							
chr10	42725029	A	T	8.5	4	43	10.2	5	44	2.6	1	37	5.7	2	33	0.0	0	42	17.9	7	32				
chr10	42759653	G	T	0.0	0	82	0.0	0	95	0.0	0	71	5.4	5	88	1.4	2	138	0.0	0	116				
chr10	42761307	G	A	0.0	0	28	0.0	0	32	19.1	9	38	6.1	2	31	0.0	0	47	12.5	6	42				
chr10	42940591	A	C	3.6	2	54	4.0	2	48	0.0	0	43	11.3	6	47	7.5	4	49	7.5	3	37				
chr10	42940592	A	G	5.4	3	53	3.9	2	49	0.0	0	44	11.1	6	48	7.7	4	48	7.5	3	37				
chr10	42940660	C	T	2.1	1	47	7.0	3	40	6.1	2	31	12.8	6	41	0.0	0	47	9.3	4	39				
chr10	43366351	C	A	8.6	7	74	4.0	4	96	0.0	0	34	12.5	6	42	5.7	3	50	7.1	4	52				
chr10	43366361	G	A	5.2	4	73	2.0	2	97	0.0	0	35	11.5	6	46	5.7	3	50	4.2	2	46				
chr10	43366382	G	A	0.0	0	67	0.0	0	100	0.0	0	35	8.9	5	51	4.0	2	48	4.8	2	40				
chr10	43594961	A	T	0.0	0	9	0.0	0	16	12.1	4	29	13.6	3	19	0.0	0	31	16.7	6	30				
chr10	66407677	A	T	0.0	0	34	0.0	0	44	10.3	3	26	32.4	11	23	0.0	0	50	0.0	0	56				
chr10	66407678	A	C	0.0	0	36	0.0	0	44	13.0	3	20	37.9	11	18	0.0	0	51	0.0	0	56				
chr10	70600322	T	A	20.8	5	19	22.6	7	24	5.7	2	33	9.4	3	29	31.0	9	20	46.4	13	15				
chr10	72430862	T	A	0.0	0	40	10.8	4	33	16.7	5	25	16.0	4	21	31.0	13	29	37.9	11	18				
chr10	83353697	C	A	20.0	4	16	5.3	1	18	0.0	0	32	19.0	4	17	6.1	2	31	11.5	3	23				
chr10	83353706	T	C	0.0	0	16	0.0	0	18	0.0	0	32	20.0	4	16	6.1	2	31	7.4	2	25				
chr10	86057597	C	A	5.1	2	37	9.5	4	38	10.3	3	26	10.0	2	18	0.0	0	38	20.0	5	20				
chr10	8723427	T	C	0.0	0	23	14.3	4	24	4.8	1	20	0.0	0	32	0.0	0	41	0.0	0	37				
chr10	89419665	C	T	0.0	0	29	0.0	0	20	0.0	0	24	17.9	7	32	12.5	4	28	8.6	3	32				
chr10	94369023	C	G	0.0	0	19	5.3	2	36	0.0	0	32	18.6	8	35	6.1	3	46	9.4	3	29				
chr10	95321679	G	A	0.0	0	40	2.9	1	33	3.1	1	31	9.8	4	37	5.4	2	35	3.7	1	26				
chr10	95321680	A	G	0.0	0	40	0.0	0	34	3.2	1	30	10.0	4	36	8.3	3	33	0.0	0	27				
chr10	96785	T	C	0.0	0	57	2.8	1	35	0.0	0	31	20.0	9	36	0.0	0	42	7.7	3	36				
chr11	10332196	C	G	29.1	16	39	17.0	9	44	32.0	8	17	34.5	10	19	3.1	1	31	7.1	3	39				
chr11	128460487	A	T	0.0	0	30	0.0	0	38	0.0	0	25	0.0	0	46	0.0	0	46	0.0	0	45				
chr11	129545864	A	T	0.0	0	38	0.0	0	33	4.7	2	41	6.3	2	30	0.0	0	45	13.3	4	26				
chr11	134805740	A	G	8.8	6	62	1.7	1	57	0.0	0	32	12.1	4	29	0.0	0	31	0.0	0	32				
chr11	1691961	T	C	1.0	4	413	0.3	1	332	3.5	6	164	4.5	10	212	4.3	12	268	4.5	11	231				
chr11	186635	C	G	0.0	0	38	20.0	13	52	11.4	9	70	16.7	12	60	7.4	5	63	3.3	1	29				
chr11	196578	C	A	0.0	0	34	14.0	6	37	1.8	1	56	2.3	1	42	5.0	3	57	6.1	2	31				
chr11	3492203	C	T	0.0	0	39	10.0	5	45	31.3	5	11	25.0	4	12	3.4	1	28	6.1	2	31				
chr11	3492227	A	C	0.0	0	37	8.9	5	51	28.6	4	10	18.8	3	13	0.0	0	29	3.3	1	29				
chr11	3509482	C	T	15.0	9	51	8.7	6	63	0.0	0	35	16.0	8	42	7.0	4	53	9.8	5	46				
chr11	357990	C	T	0.0	0	125	0.0	0	118	25.0	7	21	19.4	7	29	15.4	6	33	25.0	8	24				
chr11	37656463	A	T	0.0	0	38	9.6	5	47	0.0	0	28	3.3	1	29	0.0	0	40	0.0	0	38				
chr11	43183634	C	T	0.0	0	64	14.5	8	47	10.5	4	34	5.4	3	53	8.5	4	43	7.9	3	35				
chr11	4349708	C	T	0.0	0	28	0.0	0	39	0.0	0	42	15.8	6	32	1.3	1	76	0.0	0	59				
chr11	44441149	G	A	1.1	1	86	0.0	0	65	3.6	1	27	28.2	11	28	0.0	0	50	0.0	0	42				
chr11	48362509	A	G	11.1	7	56	4.0	2	48	5.9	2	32	22.9	8	27	0.0	0	46	15.0	6	34				
chr11	49523355	C	G	0.0	0	43	0.0	0	64	0.0	0	34	0.0	0	32	0.0	0	49	9.1	4	40				
chr11	49563925	C	T	0.0	0	9	0.0	0	16	0.0	0	35	0.0	0	23	0.0	0	27	10.8	4	33				
chr11	51584153	C	G	1.0	3	308	2.2	8	349	2.2	8	359	2.7	10	354	1.5	5	318	2.7	8	288				
chr11	5274839	T	C	0.0	0	49	2.4	1	41	45.5	10	12	43.2	16	21	0.0	0	50	8.7	4	42				
chr11	67475896	T	G	0.0	0	15	0.0	0	22	7.1	2	26	30.0	9	21	29.0	9	22	29.3	12	29				
chr11	67543327	G	A	17.1	12	58	13.9	10	62	3.1	1	31	7.7	2	24	0.0	0	53	12.8	5	34				
chr11	67543615	A	G	16.2	11	57	13.8	11	69	10.5	4	34	13.3	6	39	0.0	0	55	7.0	4	53				
chr11	67548046	C	G	11.5	7	54	17.4	12	57	4.2	1	23	19.5	8	33	0.0	0	35	26.3	10	28				

				Subject 1					Subject 2					Subject 3							
chr11	67548707	C	T	0.0	0	30	0.0	0	44	0.0	0	45	23.8	10	32	0.0	0	43	0.0	0	37
chr11	67640205	T	C	0.0	0	31	2.0	1	49	0.0	0	18	20.8	5	19	7.4	2	25	3.1	1	31
chr11	68672276	T	C	63.2	12	7	67.6	25	12	66.7	10	5	76.0	19	6	11.9	5	37	33.3	9	18
chr11	71509113	A	G	0.0	0	47	0.0	0	43	0.0	0	34	16.7	6	30	2.4	1	41	0.0	0	24
chr11	80883518	A	G	0.0	0	40	13.3	6	39	9.1	2	20	7.1	2	26	9.8	4	37	5.6	2	34
chr11	92683870	T	C	0.0	0	62	0.0	0	49	0.0	0	46	0.0	0	43	13.9	5	31	25.6	10	29
chr11	95767572	A	T	6.1	2	31	10.8	4	33	10.7	3	25	33.3	12	24	0.0	0	50	0.0	0	37
chr12	10589621	G	A	0	1	0	0	1	0	0	4	0	0	5	0	9.1	3	30	24.0	6	19
chr12	107035749	C	A	0.0	0	28	24.1	7	22	55.6	20	16	33.3	8	16	0.0	0	35	0.0	0	41
chr12	107035751	A	C	0.0	0	27	20.7	6	23	57.1	20	15	33.3	8	16	0.0	0	35	0.0	0	41
chr12	108810449	G	A	0.0	0	24	33.3	6	12	30.0	3	7	35.7	5	9	0.0	0	15	0.0	0	13
chr12	11179811	C	G	29.6	8	19	19.1	9	38	0.0	0	22	21.1	8	30	20.0	6	24	15.6	5	27
chr12	114810788	C	T	20.0	8	32	24.3	9	28	17.4	4	19	35.1	13	24	19.4	7	29	16.3	7	36
chr12	114810790	C	T	17.5	7	33	22.2	8	28	16.7	4	20	35.9	14	25	16.2	6	31	16.7	7	35
chr12	114810794	C	T	18.2	8	36	19.5	8	33	17.4	4	19	34.2	13	25	16.2	6	31	22.7	10	34
chr12	117799665	C	T	6.3	2	30	0.0	0	47	0.0	0	23	20.0	6	24	33.3	10	20	25.8	8	23
chr12	128232136	T	C	28.3	13	33	23.1	6	20	0.0	0	25	16.1	5	26	10.7	3	25	40.6	13	19
chr12	132871264	A	G	23.1	9	30	38.6	17	27	0.0	0	25	27.0	10	27	10.6	5	42	18.9	7	30
chr12	22328263	C	A	0.0	0	21	0.0	0	21	5.0	1	19	27.3	9	24	0.0	0	31	0.0	0	17
chr12	23805983	T	C	14.3	7	42	15.0	9	51	4.0	1	24	25.0	6	18	0.0	0	42	25.0	7	21
chr12	33377400	A	G	0.0	0	79	5.6	4	68	0.0	0	30	0.0	0	47	0.0	0	57	0.0	0	41
chr12	34185354	A	G	0.0	0	24	0.0	0	31	0.0	0	37	0.0	0	19	0.0	0	33	11.8	4	30
chr12	34185356	T	C	0.0	0	24	0.0	0	31	0.0	0	36	0.0	0	18	0.0	0	32	11.4	4	31
chr12	34185385	A	C	0.0	0	23	0.0	0	34	0.0	0	30	4.3	1	22	0.0	0	34	11.8	4	30
chr12	34325981	T	C	0.0	0	35	0.0	0	38	0.0	0	40	7.5	4	49	2.7	2	73	4.8	2	40
chr12	34343131	T	G	0.0	0	38	0.0	0	39	4.9	2	39	0.0	0	29	0.0	0	58	8.9	4	41
chr12	34345941	G	A	7.0	3	40	7.7	3	36	2.3	1	43	10.0	3	27	0.0	0	41	16.3	7	36
chr12	34345950	T	C	7.1	3	39	7.3	3	38	4.4	2	43	6.3	2	30	0.0	0	41	13.3	6	39
chr12	3599001	G	A	0.0	0	60	7.7	4	48	0.0	0	38	3.2	1	30	3.7	2	52	2.4	1	40
chr12	37862133	A	T	22.2	6	21	13.3	4	26	0.0	0	19	16.7	6	30	3.2	1	30	11.8	2	15
chr12	37877384	G	A	0.0	0	52	8.2	5	56	1.8	1	55	6.1	3	46	3.7	3	78	1.8	1	55
chr12	37911376	A	G	6.1	3	46	5.5	3	52	0.0	0	28	10.3	4	35	0.0	0	54	5.3	2	36
chr12	37911392	T	G	10.2	5	44	15.7	8	43	0.0	0	32	14.3	5	30	1.9	1	53	4.9	2	39
chr12	37911703	C	G	10.3	3	26	20.6	7	27	5.3	1	18	4.8	1	20	12.1	4	29	13.8	4	25
chr12	37953515	G	A	0.0	0	41	10.5	6	51	2.7	1	36	4.5	2	42	0.0	0	47	0.0	0	36
chr12	37953539	A	C	0.0	0	45	9.3	5	49	2.9	1	34	2.6	1	38	0.0	0	48	0.0	0	36
chr12	38592498	C	T	0.0	0	115	0.0	0	117	4.8	6	119	2.6	4	148	0.6	1	175	6.5	10	144
chr12	38594227	G	A	8.6	13	138	10.9	14	115	1.5	1	67	6.6	6	85	5.1	5	93	8.0	7	81
chr12	38594721	G	T	9.7	7	65	4.2	3	69	2.8	2	69	3.3	4	117	0.7	1	139	5.6	6	101
chr12	54316131	A	G	2.9	1	33	17.6	6	28	0.0	0	33	0.0	0	40	0.0	0	36	0.0	0	44
chr12	5491298	T	G	23.3	7	23	27.1	16	43	19.1	9	38	11.4	5	39	1.8	1	54	35.1	13	24
chr12	65872230	C	T	9.1	3	30	3.8	2	50	3.1	1	31	8.8	3	31	0.0	0	33	12.5	7	49
chr12	72617891	T	C	0.0	0	35	9.4	5	48	0.0	0	22	0.0	0	29	14.3	4	24	4.3	1	22
chr12	82163	C	A	0.7	1	134	0.8	1	130	1.7	1	59	2.5	2	77	2.8	2	70	17.7	11	51
chr12	84110729	T	G	0	25	0	0	31	0	25.0	8	24	42.1	16	22	0	31	0	0	27	0
chr12	8422566	G	A	0.0	0	50	0.0	0	53	0.0	0	32	14.3	5	30	5.7	2	33	11.4	4	31
chr12	86115457	C	A	0.0	0	41	0.0	0	42	0.0	0	23	0.0	0	26	0.0	0	38	14.3	4	24

				Subject 1						Subject 2						Subject 3					
chr12	86738536	G	A	2.7	1	36	4.8	2	40	2.9	1	33	40.9	9	13	0.0	0	47	0.0	0	25
chr12	92852756	C	T	8.7	2	21	2.9	1	34	0.0	0	26	11.8	4	30	16.1	5	26	9.1	3	30
chr12	98113980	A	G	11.1	3	24	18.2	6	27	10.7	3	25	27.8	10	26	20.0	7	28	22.4	11	38
chr13	111133489	A	G	41.5	44	62	45.2	52	63	50.0	4	4	30.8	4	9	3.1	1	31	29.6	8	19
chr13	113443808	G	C	0.0	0	35	17.6	6	28	0.0	0	22	0.0	0	30	0.0	0	41	0.0	0	16
chr13	113443846	C	T	0.0	0	53	12.8	5	34	0.0	0	22	0.0	0	30	0.0	0	35	0.0	0	24
chr13	114519180	G	T	13.2	20	131	16.5	22	111	6.8	3	41	11.1	5	40	5.2	3	55	22.4	11	38
chr13	19098162	C	T	0.0	0	35	24.1	7	22	2.5	1	39	3.1	1	31	6.5	2	29	3.1	1	31
chr13	19099122	C	A	0.0	0	34	0.0	0	44	2.4	1	40	19.7	12	49	0.0	0	30	0.0	0	58
chr13	19099139	C	T	0.0	0	43	0.0	0	52	2.2	1	44	19.0	12	51	35.3	12	22	14.8	9	52
chr13	19320805	C	G	19.1	13	55	14.3	9	54	0.0	0	24	25.0	8	24	12.5	5	35	14.3	5	30
chr13	19348798	A	G	0.0	0	37	8.5	4	43	6.3	1	15	7.4	2	25	6.3	2	30	0.0	0	30
chr13	19448238	T	C	4.0	3	72	14.3	12	72	14.7	10	58	18.0	11	50	10.4	8	69	16.9	14	69
chr13	25154565	G	C	2.0	1	48	0.0	0	49	0.0	0	38	14.3	5	30	13.9	5	31	6.1	2	31
chr13	26035990	A	G	11.8	4	30	9.4	3	29	4.8	1	20	35.7	10	18	22.7	10	34	21.4	6	22
chr13	26823944	G	A	6.8	3	41	24.6	16	49	31.6	12	26	29.5	13	31	1.8	1	54	4.3	2	45
chr13	27904494	T	C	0.0	0	41	0.0	0	34	0.0	0	27	0.0	0	22	3.4	1	28	17.6	6	28
chr13	50460236	G	T	0.0	0	13	7.4	2	25	13.3	4	26	35.7	10	18	0.0	0	32	0.0	0	22
chr13	56230379	C	A	0.0	0	55	19.4	12	50	0.0	0	35	4.0	1	24	10.5	6	51	8.5	4	43
chr13	56851807	G	A	26.3	10	28	27.8	10	26	25.0	5	15	15.4	6	33	4.5	1	21	40.6	13	19
chr13	70411802	G	A	0.0	0	23	16.7	5	25	21.2	7	26	50.0	7	7	35.7	5	9	50.0	7	7
chr13	81442677	C	T	0.0	0	5	12.5	1	7	0.0	0	28	0.0	0	15	19.0	4	17	18.5	5	22
chr13	83178220	C	T	11.4	4	31	5.6	2	34	0.0	0	39	0.0	0	30	31.3	15	33	25.0	12	36
chr13	83178222	C	T	11.4	4	31	5.6	2	34	0.0	0	39	0.0	0	29	31.3	15	33	26.1	12	34
chr13	92456262	A	C	2.0	1	50	8.6	5	53	0.0	0	35	14.6	6	35	4.1	2	47	2.4	1	41
chr14	104691815	G	A	3.4	1	28	0.0	0	20	0.0	0	33	10.8	4	33	0.0	0	34	0.0	0	41
chr14	104755598	G	T	5.0	18	345	3.9	16	390	0.0	0	44	7.7	4	48	0.0	0	54	2.9	1	33
chr14	106193938	G	A	28.6	26	65	32.0	32	68	19.4	7	29	25.0	11	33	18.6	11	48	23.7	14	45
chr14	106715231	A	T	2.3	1	42	0.0	0	53	0.0	0	29	17.4	8	38	0.0	0	48	0.0	0	42
chr14	106813803	G	A	7.4	7	87	15.0	16	91	0.0	0	47	9.3	5	49	15.7	8	43	24.0	6	19
chr14	106824844	C	T	0.0	0	69	0.0	0	70	0.0	0	40	7.3	4	51	24.4	10	31	5.7	3	50
chr14	107086705	C	G	0.0	0	22	0.0	0	28	12.5	2	14	4.5	1	21	4.7	2	41	11.8	4	30
chr14	107129606	A	G	0.0	0	39	0.0	0	32	0.0	0	34	0.0	0	27	0.0	0	36	11.8	4	30
chr14	107282577	C	T	0.0	0	65	6.9	6	81	0.0	0	44	0.0	0	39	3.8	2	50	4.3	2	44
chr14	107282578	A	G	0.0	0	65	5.8	5	81	4.5	2	42	7.5	3	37	11.3	6	47	6.8	3	41
chr14	107282596	T	C	0.0	0	61	7.7	6	72	5.4	2	35	9.8	4	37	7.8	4	47	6.8	3	41
chr14	19023794	G	A	6.7	5	70	6.3	5	74	1.6	1	62	9.2	8	79	5.3	5	90	5.5	5	86
chr14	19026816	A	G	0.0	0	109	1.0	1	96	0.0	0	68	5.8	5	81	0.0	0	119	4.6	5	103
chr14	19026822	T	C	0.0	0	113	1.1	1	94	0.0	0	71	5.7	5	82	0.8	1	123	4.5	5	106
chr14	19027305	G	A	1.8	3	165	2.9	5	168	0.8	1	129	5.0	6	113	1.5	3	199	0.7	1	151
chr14	19096453	T	C	0.8	1	126	3.9	5	122	1.5	1	65	2.4	2	83	1.2	1	84	2.3	2	84
chr14	19112525	G	A	0.0	0	72	1.0	1	95	3.8	2	51	1.5	1	67	0.0	0	71	6.3	4	60
chr14	19112671	A	G	4.9	3	58	7.0	5	66	1.6	1	60	12.5	8	56	6.7	6	83	14.9	10	57
chr14	19124230	C	T	12.4	13	92	12.6	13	90	3.6	2	54	5.8	4	65	9.1	8	80	7.4	6	75
chr14	20019255	G	T	0.0	0	21	18.6	8	35	25.0	8	24	12.8	5	34	1.2	1	83	0.0	0	52
chr14	20139079	A	G	0	30	0	0	39	0	0.0	0	27	15.6	5	27	47.7	21	23	59.1	26	18
chr14	20277085	T	A	0.0	0	43	6.8	4	55	0.0	0	26	0.0	0	24	0.0	0	66	0.0	0	62

				Subject 1					Subject 2					Subject 3							
chr14	24441235	A	T	6.1	3	46	8.0	4	46	0.0	0	27	15.0	3	17	5.3	2	36	0.0	0	24
chr14	28320841	G	C	1.8	1	54	0.0	0	48	0.0	0	45	12.0	6	44	8.6	6	64	9.4	6	58
chr14	32357497	C	T	0.0	0	33	0.0	0	42	0.0	0	21	23.1	3	10	10.3	3	26	10.3	3	26
chr14	64895988	C	A	3.0	1	32	10.0	3	27	0.0	0	26	0.0	0	35	16.1	5	26	18.2	6	27
chr14	71946053	G	T	10.9	7	57	21.4	15	55	3.7	1	26	22.2	10	35	36.7	18	31	26.2	11	31
chr14	77192388	A	G	28.4	19	48	33.3	22	44	20.0	4	16	39.1	9	14	19.0	4	17	28.1	9	23
chr14	96077177	G	A	0.0	0	52	1.3	1	76	3.3	1	29	2.4	1	40	0.0	0	35	13.5	5	32
chr14	96077179	A	G	0.0	0	52	0.0	0	75	0.0	0	30	0.0	0	40	0.0	0	35	11.1	4	32
chr15	101105491	T	G	0.0	0	24	0.0	0	40	14.3	3	18	23.3	7	23	43.3	13	17	20.0	7	28
chr15	20027630	C	T	4.2	2	46	2.5	1	39	0.0	0	57	13.8	8	50	10.0	7	63	5.5	3	52
chr15	20054213	C	A	16.1	5	26	27.3	6	16	13.0	3	20	25.9	7	20	0.0	0	34	39.1	9	14
chr15	20056535	C	T	23.5	4	13	31.8	7	15	0.0	0	18	11.5	3	23	0.0	0	34	11.5	3	23
chr15	20081632	G	A	23.1	6	20	23.3	7	23	0.0	0	29	25.0	4	12	0.0	0	43	0.0	0	35
chr15	20084861	C	T	0.0	0	31	28.6	12	30	32.5	13	27	20.5	8	31	20.0	7	28	26.5	9	25
chr15	20084864	T	A	0.0	0	30	28.6	12	30	28.9	11	27	18.4	7	31	19.4	7	29	25.7	9	26
chr15	20085443	T	C	15.4	6	33	23.7	9	29	3.8	1	25	25.0	6	18	17.4	8	38	26.9	7	19
chr15	20108463	A	G	7.4	10	126	3.2	5	151	1.0	1	100	4.6	5	104	4.4	5	108	5.7	5	82
chr15	20110035	T	A	10.3	7	61	5.6	3	51	4.1	2	47	15.6	10	54	15.2	5	28	8.9	4	41
chr15	20110557	G	T	3.3	3	88	5.7	7	116	1.3	2	155	4.2	7	159	5.6	9	153	2.9	4	134
chr15	20116044	C	T	3.3	1	29	5.0	2	38	24.1	7	22	12.9	4	27	0.0	0	38	13.5	5	32
chr15	20175455	G	C	0.0	0	46	7.8	5	59	11.8	4	30	7.3	3	38	4.8	3	59	3.4	2	56
chr15	20461435	A	G	0.0	0	111	0.0	0	90	8.5	6	65	4.5	3	63	1.4	1	70	11.0	8	65
chr15	20473814	G	A	0.0	0	103	0.0	0	107	1.4	1	73	7.9	6	70	0.0	0	78	9.5	8	76
chr15	20527417	T	C	0.0	0	67	12.3	8	57	5.1	4	75	8.0	7	80	13.1	11	73	13.8	9	56
chr15	20537900	C	A	0.0	0	40	1.9	1	51	0.0	0	42	10.5	4	34	2.1	1	47	4.1	2	47
chr15	22830920	C	G	0.0	0	99	1.0	1	99	0.0	0	55	0.0	0	61	1.3	1	75	11.1	5	40
chr15	24412318	T	G	0.0	0	34	7.1	2	26	0.0	0	35	15.6	7	38	0.0	0	36	2.6	1	38
chr15	24412338	G	A	0.0	0	34	6.9	2	27	0.0	0	39	15.4	6	33	56.8	21	16	55.6	20	16
chr15	24412345	C	T	0.0	0	32	0.0	0	31	0.0	0	38	16.7	6	30	0.0	0	38	0.0	0	39
chr15	24415855	A	T	1.6	1	61	1.9	1	52	4.4	2	43	12.5	4	28	0.0	0	57	13.3	6	39
chr15	24415875	T	C	0.0	0	58	0.0	0	49	2.3	1	42	3.4	1	28	0.0	0	67	13.0	6	40
chr15	24478365	A	C	0.0	0	35	0.0	0	36	0.0	0	22	3.7	1	26	0.0	0	44	12.2	6	43
chr15	24667102	C	A	12.3	8	57	1.9	1	52	5.3	2	36	0.0	0	39	0.0	0	50	10.5	4	34
chr15	24672635	A	C	0.0	0	15	0.0	0	16	0.0	0	50	0.0	0	55	0.0	0	48	14.3	5	30
chr15	24716617	C	T	0.0	0	33	0.0	0	51	23.3	7	23	16.7	4	20	2.9	2	68	20.0	10	40
chr15	24716623	T	C	0.0	0	36	0.0	0	55	25.0	7	21	13.3	4	26	4.3	3	67	21.3	10	37
chr15	24771136	T	C	0.0	0	44	0.0	0	61	0.0	0	32	11.4	4	31	6.5	5	72	3.4	2	56
chr15	24790912	A	G	0.0	0	21	0.0	0	33	0.0	0	30	12.5	4	28	2.2	1	45	0.0	0	23
chr15	24790956	C	G	0.0	0	26	0.0	0	38	0.0	0	31	12.1	4	29	0.0	0	46	0.0	0	30
chr15	24790965	A	G	0.0	0	28	0.0	0	36	0.0	0	29	12.5	4	28	0.0	0	43	0.0	0	29
chr15	24796809	C	A	0.0	0	39	2.3	1	42	0.0	0	35	9.5	4	38	0.0	0	43	2.4	1	40
chr15	29055776	A	G	0.0	0	37	0.0	0	35	0.0	0	26	0.0	0	26	0.0	0	49	14.7	5	29
chr15	40043619	A	C	15.4	6	33	32.3	10	21	3.7	1	26	0.0	0	40	12.2	6	43	7.3	3	38
chr15	41438167	A	G	0.0	0	34	23.8	5	16	10.5	2	17	17.6	3	14	0.0	0	31	4.0	1	24
chr15	45497720	T	C	15.9	10	53	18.2	12	54	0.0	0	30	19.4	7	29	12.5	8	56	28.6	12	30
chr15	45497721	C	T	20.6	13	50	24.2	16	50	0.0	0	31	18.9	7	30	12.5	8	56	28.6	12	30
chr15	45497724	C	T	18.0	11	50	24.2	16	50	0.0	0	30	18.9	7	30	28.8	19	47	37.2	16	27

				Subject 1						Subject 2						Subject 3					
chr15	47351250	T	G	0.0	0	40	9.8	4	37	0.0	0	30	3.2	1	30	3.9	2	49	3.7	1	26
chr15	47352177	A	G	0.0	0	37	18.8	9	39	21.1	8	30	11.9	5	37	9.7	6	56	7.9	3	35
chr15	47373545	G	A	0.0	0	64	0.0	0	52	3.3	1	29	7.9	3	35	2.0	1	48	12.5	3	21
chr15	47376986	T	A	0.0	0	50	2.1	1	47	0.0	0	32	0.0	0	22	0.0	0	45	8.9	4	41
chr15	47376987	T	C	0.0	0	51	2.0	1	48	0.0	0	32	0.0	0	22	0.0	0	45	8.5	4	43
chr15	47377015	G	A	0.0	0	54	0.0	0	44	0.0	0	29	0.0	0	22	0.0	0	49	10.4	5	43
chr15	54998318	A	G	71.4	30	12	79.6	39	10	38.7	12	19	45.5	10	12	70.4	38	16	76.7	33	10
chr15	58906500	A	T	30.0	15	35	27.3	9	24	15.6	5	27	27.3	9	24	13.0	6	40	16.2	6	31
chr15	63822482	C	T	47.1	16	18	61.1	22	14	73.9	17	6	88.5	23	3	44.1	15	19	48.3	14	15
chr15	69647687	C	T	0.0	0	26	17.1	6	29	0.0	0	24	0.0	0	18	0.0	0	25	0.0	0	35
chr15	73666025	G	A	10.0	1	9	9.1	1	10	24.0	6	19	26.1	6	17	6.9	2	27	25.9	7	20
chr15	77397695	T	C	37.8	14	23	40.4	21	31	40.9	9	13	53.6	15	13	9.7	3	28	31.6	12	26
chr15	77397697	T	C	23.7	9	29	15.4	8	44	40.9	9	13	50.0	13	13	9.7	3	28	31.7	13	28
chr15	86386720	G	C	4.0	6	145	6.0	9	141	0.0	0	31	2.2	1	44	0.0	0	52	0.0	0	40
chr15	91701963	C	T	4.5	3	63	20.7	12	46	0.0	0	25	0.0	0	25	20.0	10	40	8.3	3	33
chr15	98585072	C	T	14.8	20	115	16.5	22	111	0.0	0	28	0.0	0	30	2.7	2	71	23.1	12	40
chr16	10656235	C	A	14.6	6	35	25.0	10	30	0.0	0	28	16.7	7	35	51.2	22	21	59.5	22	15
chr16	10808148	G	A	13.3	8	52	16.0	12	63	13.3	6	39	26.4	14	39	29.8	14	33	37.1	26	44
chr16	13874735	G	T	22.9	11	37	41.1	23	33	16.7	5	25	2.8	1	35	5.1	3	56	32.5	13	27
chr16	18328011	A	G	25.6	20	58	21.4	18	66	5.7	2	33	23.2	13	43	31.5	34	74	24.7	22	67
chr16	20134507	T	A	28.8	15	37	33.3	14	28	66.7	22	11	54.3	19	16	24.4	11	34	42.1	16	22
chr16	22674364	T	C	0.0	0	65	8.1	5	57	14.8	4	23	6.5	3	43	10.8	4	33	9.3	4	39
chr16	24913279	G	A	1.7	1	57	10.4	5	43	60.0	18	12	58.1	25	18	11.9	5	37	26.7	8	22
chr16	25227401	C	T	2.7	1	36	12.5	5	35	5.6	1	17	9.1	2	20	18.2	6	27	46.2	6	7
chr16	27958857	T	A	3.2	1	30	14.0	6	37	4.8	1	20	22.6	7	24	2.3	1	42	13.2	5	33
chr16	27958861	G	A	9.7	3	28	9.5	4	38	5.6	1	17	30.3	10	23	0.0	0	35	0.0	0	39
chr16	29126761	A	C	4.5	4	84	3.0	2	65	0.0	0	33	9.5	4	38	4.9	2	39	0.0	0	37
chr16	2938026	A	T	0.0	0	37	0.0	0	56	20.7	6	23	26.2	11	31	4.1	2	47	25.5	12	35
chr16	30658538	A	G	0.0	0	25	0.0	0	21	0.0	0	26	0.0	0	19	0.0	0	34	24.0	6	19
chr16	3209538	T	C	3.1	1	31	8.3	2	22	0.0	0	25	0.0	0	24	0.0	0	33	13.3	4	26
chr16	32113113	A	T	0.0	0	48	11.1	5	40	0.0	0	58	0.0	0	54	0.0	0	47	0.0	0	39
chr16	32113129	T	C	0.0	0	49	12.5	6	42	1.5	1	64	3.7	2	52	5.8	3	49	2.4	1	40
chr16	32119584	T	C	17.5	7	33	9.6	5	47	0.0	0	40	10.2	5	44	8.5	5	54	20.5	9	35
chr16	32119618	A	C	12.1	7	51	6.8	5	69	1.5	1	64	7.4	5	63	7.1	5	65	17.0	9	44
chr16	32119623	G	T	12.3	7	50	8.3	6	66	1.6	1	62	7.1	5	65	7.1	5	65	18.4	9	40
chr16	32290384	A	C	5.8	6	98	4.3	4	88	7.8	5	59	6.9	5	67	0.0	0	96	10.8	7	58
chr16	32370720	A	T	17.6	6	28	15.6	7	38	0.0	0	73	9.4	8	77	3.4	4	114	5.5	7	120
chr16	32370731	G	A	20.6	7	27	10.0	4	36	0.0	0	74	7.8	6	71	3.6	4	108	6.3	7	105
chr16	32399267	T	G	13.6	6	38	9.3	4	39	7.5	4	49	19.7	13	53	27.4	34	90	33.3	30	60
chr16	32440208	C	T	2.9	1	33	7.5	3	37	16.7	9	45	23.7	9	29	5.4	5	88	17.1	12	58
chr16	32440219	C	A	23.3	10	33	13.2	5	33	17.0	9	44	21.6	8	29	3.1	3	93	12.1	8	58
chr16	32448632	A	C	2.9	1	33	9.5	4	38	1.4	1	70	5.8	4	65	2.0	2	98	6.9	7	94
chr16	32452713	C	A	25.0	19	57	44.1	26	33	2.5	1	39	19.2	15	63	17.3	17	81	26.1	18	51
chr16	32495421	A	C	0.0	0	32	0.0	0	49	0.0	0	45	7.8	6	71	1.0	1	98	4.1	3	71
chr16	32497908	T	A	0.0	0	51	0.0	0	45	1.4	1	68	7.2	7	90	0.0	0	142	0.0	0	84
chr16	32822280	G	C	2.0	3	145	5.3	7	125	7.0	7	93	2.5	3	118	0.0	0	126	8.0	7	81
chr16	32822286	G	C	2.0	3	145	5.6	7	119	8.7	8	84	2.5	3	117	0.0	0	123	6.7	6	83

				Subject 1					Subject 2					Subject 3											
				G	T	2.1	3	138	7.0	8	106	9.4	9	87	0.0	0	114	0.8	1	122	6.3	5	74		
chr16	32822320	G	T	2.1	3	138	7.0	8	106	9.4	9	87	0.0	0	137	5.1	7	129	5.5	8	138	2.7	3	110	
chr16	32830915	G	T	0.8	1	129	1.3	2	148	0.0	0	137	5.1	7	129	5.5	8	138	2.7	3	110				
chr16	32841338	T	A	7.4	5	63	6.8	4	55	0.0	0	79	7.0	5	66	0.0	0	92	0.0	0	92	0.0	0	81	
chr16	33044932	G	A	2.7	4	143	2.6	4	149	6.3	4	59	4.1	6	139	1.6	2	123	9.6	16	151				
chr16	33045710	A	T	'NA'	'NA'	'NA'	'NA'	33.3	1	2	28.6	4	10	31.3	5	11	0.0	0	20	17.6	6	28			
chr16	33369419	C	A	1.2	1	84	6.1	5	77	6.7	6	83	4.1	3	71	3.8	5	128	7.8	9	107				
chr16	33443607	T	C	10.3	4	35	15.2	7	39	1.6	1	60	12.5	12	84	8.7	9	95	7.7	6	72				
chr16	33452282	G	A	17.3	9	43	11.9	7	52	0.0	0	27	15.1	8	45	4.9	3	58	9.1	7	70				
chr16	33518644	C	T	9.3	12	117	9.0	12	122	0.0	0	98	7.5	8	99	6.3	8	119	12.2	16	115				
chr16	33578122	T	G	2.3	1	43	7.3	3	38	0.0	0	61	8.3	5	55	1.0	1	99	5.7	4	66				
chr16	33583348	A	G	17.4	8	38	11.8	6	45	0.0	0	77	7.7	5	60	8.8	10	103	9.1	8	80				
chr16	33590053	A	C	2.6	1	38	3.4	2	57	2.5	2	79	0.0	0	58	0.0	0	93	7.8	6	71				
chr16	33833766	A	T	0.0	0	48	0.0	0	61	0.0	0	40	9.1	5	50	0.0	0	63	1.8	1	56				
chr16	33838938	A	G	12.2	6	43	0.0	0	50	9.1	3	30	19.4	7	29	2.0	1	49	18.0	9	41				
chr16	33901480	C	T	4.6	7	144	10.4	17	147	2.9	3	102	13.2	18	118	10.8	18	149	12.1	16	116				
chr16	33916009	C	T	9.9	11	100	2.2	2	87	1.0	1	103	4.2	5	115	3.7	6	156	8.3	13	143				
chr16	33979543	G	A	5.6	7	118	5.2	6	109	0.0	0	105	4.9	5	98	7.2	13	168	7.0	12	159				
chr16	34179570	T	C	10.2	6	53	9.9	8	73	3.7	2	52	10.2	5	44	4.1	3	71	8.5	5	54				
chr16	34180186	C	T	13.4	22	142	11.2	24	191	1.8	3	162	6.8	9	123	7.4	15	189	4.6	7	144				
chr16	34407027	C	T	0.0	0	67	0.0	0	71	0.0	0	41	0.0	0	43	0.0	0	53	7.8	4	47				
chr16	46456468	G	C	12.2	18	129	6.9	11	148	12.5	8	56	6.7	6	83	0.0	0	123	12.0	10	73				
chr16	46456469	G	A	9.9	14	128	6.2	10	152	14.3	9	54	6.7	6	84	0.8	1	120	11.0	9	73				
chr16	46456604	C	G	4.5	5	106	3.1	4	124	0.0	0	65	6.9	6	81	4.8	6	119	3.1	3	94				
chr16	46464355	T	G	2.2	1	45	3.4	2	56	0.0	0	47	11.9	7	52	5.3	4	71	3.1	2	62				
chr16	46489595	A	G	0.0	0	26	22.5	9	31	23.1	12	40	28.0	7	18	16.1	5	26	18.2	8	36				
chr16	46492182	C	T	1.3	3	231	4.6	10	206	5.7	8	133	3.8	6	150	5.9	12	192	6.1	11	168				
chr16	46493939	G	T	6.1	7	108	3.5	6	164	3.3	4	117	3.2	4	120	0.0	0	124	5.9	7	111				
chr16	46493946	A	G	6.7	7	97	2.6	4	151	3.6	4	107	3.4	4	113	0.9	1	114	5.6	6	102				
chr16	46494681	T	C	2.9	2	67	8.1	7	79	5.6	5	84	3.8	3	77	4.0	3	72	4.5	4	85				
chr16	52058940	T	C	0.0	0	37	0.0	0	49	0.0	0	20	31.8	7	15	0.0	0	44	0.0	0	27				
chr16	54474166	T	C	0.0	0	29	0.0	0	22	0.0	0	21	0.0	0	25	3.7	1	26	18.2	4	18				
chr16	74588388	T	C	0.0	0	42	2.1	1	46	0.0	0	49	10.0	6	54	0.0	0	66	6.3	3	45				
chr16	83700441	T	C	23.7	14	45	10.9	5	41	20.7	6	23	30.8	8	18	0.0	0	58	2.0	1	49				
chr16	87812073	T	C	17.4	8	38	11.6	5	38	16.7	5	25	21.6	8	29	0.0	0	41	2.9	1	33				
chr16	89020741	C	G	0.0	0	33	0.0	0	46	0.0	0	18	7.7	1	12	0.0	0	31	12.5	4	28				
chr16	90152902	T	A	8.9	4	41	1.7	1	57	3.0	1	32	12.5	4	28	7.2	5	64	5.0	2	38				
chr16	90159640	C	T	5.7	5	82	12.8	11	75	0.0	0	57	7.7	7	84	13.8	11	69	2.4	2	82				
chr17	17424880	A	T	0.0	0	44	12.0	6	44	2.9	1	33	0.0	0	41	8.5	5	54	0.0	0	40				
chr17	21387576	G	A	10.0	5	45	3.7	2	52	0.0	0	41	9.5	4	38	1.7	1	58	0.0	0	39				
chr17	21514789	T	C	17.4	8	38	11.1	5	40	9.7	3	28	15.0	6	34	6.1	3	46	24.4	11	34				
chr17	21534590	A	T	2.9	1	34	4.0	2	48	18.2	12	54	3.0	1	32	0.0	0	64	7.5	5	62				
chr17	21538097	T	C	20.6	7	27	19.3	11	46	0.0	0	36	22.9	8	27	24.0	12	38	11.1	4	32				
chr17	21538123	C	T	19.4	6	25	22.4	11	38	0.0	0	39	27.8	10	26	22.2	12	42	11.8	4	30				
chr17	21553956	G	C	0.3	1	310	0.0	0	294	1.0	1	100	6.1	8	123	0.0	0	182	0.0	0	191				
chr17	21563300	C	T	0.7	1	146	0.0	0	161	0.0	0	60	6.5	6	86	6.0	8	125	4.9	5	97				
chr17	21886558	A	G	0.0	0	69	1.4	1	72	3.6	2	54	11.9	5	37	1.3	1	74	3.6	2	53				
chr17	21894590	T	C	12.8	5	34	13.3	4	26	0.0	0	31	20.4	10	39	6.7	4	56	12.0	6	44				

				Subject 1							Subject 2							Subject 3						
chr17	21894591	G	C	13.2	5	33	14.3	4	24	0.0	0	31	17.0	8	39	5.5	3	52	8.5	4	43			
chr17	22207051	G	T	10.6	11	93	17.9	17	78	6.3	2	30	5.6	2	34	0.0	0	52	7.8	4	47			
chr17	22213394	T	C	2.3	1	42	5.0	2	38	16.9	11	54	16.7	7	35	2.2	1	44	23.3	10	33			
chr17	25269328	G	A	0.0	0	47	10.0	6	54	3.2	2	60	5.8	4	65	6.2	4	61	2.3	2	86			
chr17	25276050	T	C	5.9	6	96	2.2	2	91	0.0	0	80	0.0	0	46	1.9	2	106	11.1	8	64			
chr17	25303927	T	G	0.0	0	98	5.8	9	147	0.0	0	131	0.0	0	128	0.7	1	137	6.1	11	168			
chr17	25306354	C	A	5.4	5	88	6.4	7	103	3.3	2	59	3.9	3	73	0.0	0	90	6.9	4	54			
chr17	25310785	G	A	5.5	4	69	8.5	6	65	0.0	0	31	12.8	6	41	14.0	8	49	4.1	2	47			
chr17	25313724	T	G	1.5	2	128	3.8	5	125	0.0	0	70	7.1	6	78	1.4	2	138	2.5	2	78			
chr17	25313744	A	C	0.0	0	129	0.8	1	128	0.0	0	69	6.8	6	82	1.4	2	143	1.4	1	71			
chr17	25329018	G	T	0.0	0	68	0.0	0	67	2.1	1	47	13.1	8	53	8.2	5	56	5.7	3	50			
chr17	27355087	C	T	6.0	3	47	17.0	8	39	32.0	8	17	35.7	10	18	0.0	0	47	0.0	0	24			
chr17	27355089	C	T	3.9	2	49	13.0	6	40	26.1	6	17	33.3	9	18	0.0	0	47	0.0	0	25			
chr17	28980758	T	C	0.0	0	45	13.6	6	38	0.0	0	24	0.0	0	24	0.0	0	46	0.0	0	18			
chr17	29590117	G	A	1.9	1	51	2.1	1	47	0.0	0	27	13.9	5	31	41.7	20	28	34.8	8	15			
chr17	36466214	A	G	0.0	0	40	10.5	4	34	2.9	1	34	0.0	0	33	0.0	0	40	0.0	0	41			
chr17	44329020	G	A	0.0	0	61	0.0	0	73	0.0	0	34	0.0	0	38	0.0	0	53	11.6	5	38			
chr17	5394640	A	G	46.9	23	26	56.8	21	16	0.0	0	19	45.0	9	11	39.1	9	14	48.5	16	17			
chr17	57556796	C	T	0.0	0	61	0.0	0	48	10.5	4	34	5.9	2	32	3.8	2	51	14.3	7	42			
chr17	58279083	G	A	0.0	0	33	22.2	6	21	6.7	1	14	10.0	2	18	6.1	2	31	5.9	1	16			
chr17	63332975	T	C	13.6	8	51	12.1	7	51	0.0	0	32	0.0	0	25	0.0	0	38	27.3	9	24			
chr17	63967290	G	T	23.4	18	59	17.5	14	66	0.0	0	40	0.0	0	49	13.7	7	44	23.6	13	42			
chr17	670973	G	A	15.9	7	37	8.1	3	34	0.0	0	28	16.7	5	25	4.8	2	40	7.5	3	37			
chr17	75267466	A	G	0.0	0	40	0.0	0	32	0.0	0	20	3.1	1	31	4.5	2	42	0.0	0	33			
chr17	80483780	C	G	12.8	6	41	6.3	3	45	0.0	0	25	21.7	5	18	0.0	0	39	0.0	0	42			
chr18	12121434	T	C	5.4	3	53	3.7	1	26	0.0	0	29	17.6	6	28	3.1	2	62	11.8	6	45			
chr18	12121448	T	C	5.3	3	54	2.9	1	33	0.0	0	31	20.7	6	23	3.0	2	65	13.2	7	46			
chr18	14226226	G	C	9.3	4	39	10.5	4	34	0.0	0	44	17.2	5	24	15.6	7	38	3.7	1	26			
chr18	14238162	C	T	8.2	4	45	9.8	5	46	0.0	0	36	8.7	4	42	7.8	4	47	9.3	4	39			
chr18	14407731	A	T	0.0	0	64	1.8	1	54	0.0	0	31	25.8	8	23	5.7	2	33	3.0	1	32			
chr18	14431350	G	T	8.1	5	57	2.5	1	39	14.3	3	18	20.0	6	24	0.0	0	38	16.7	6	30			
chr18	14431351	C	T	8.1	5	57	2.5	1	39	14.3	3	18	19.4	6	25	0.0	0	39	16.7	6	30			
chr18	14529224	A	G	9.1	4	40	2.8	1	35	0.0	0	42	27.8	5	13	0.0	0	42	3.6	1	27			
chr18	14554058	A	G	20.0	10	40	15.4	10	55	0.0	0	27	14.3	6	36	11.6	8	61	19.5	8	33			
chr18	14556863	T	C	9.1	4	40	2.4	1	40	2.4	1	41	2.2	1	45	4.7	2	41	13.0	6	40			
chr18	15162522	T	A	0.0	0	64	8.3	5	55	0.0	0	28	2.1	1	47	3.2	2	61	2.0	1	48			
chr18	15167433	G	C	0.0	0	138	0.8	1	125	1.0	1	96	4.7	5	101	0.8	1	130	8.9	9	92			
chr18	15168212	A	G	11.0	13	105	6.9	9	122	0.0	0	95	7.0	10	133	3.9	7	174	4.3	7	154			
chr18	15173199	C	T	0.0	0	58	4.9	4	78	1.7	1	58	5.8	5	81	1.0	1	102	4.3	3	67			
chr18	15174663	C	T	0.0	0	58	2.3	2	84	7.4	4	50	0.0	0	63	1.4	1	68	8.1	6	68			
chr18	15174675	T	A	0.0	0	37	2.9	2	67	7.1	4	52	0.0	0	60	1.5	1	64	8.2	5	56			
chr18	15176832	A	C	1.2	2	160	3.1	6	186	1.4	1	68	7.9	8	93	1.6	2	123	3.6	4	106			
chr18	15185521	T	C	8.6	3	32	27.0	10	27	3.8	1	25	6.5	2	29	0.0	0	26	19.4	7	29			
chr18	15185527	C	T	9.4	3	29	25.0	10	30	3.7	1	26	6.7	2	28	0.0	0	25	16.7	6	30			
chr18	15185546	A	G	9.7	3	28	26.3	10	28	7.1	2	26	9.7	3	28	0.0	0	26	20.0	7	28			
chr18	15300595	A	T	8.3	2	22	0.0	0	36	0.0	0	38	0.0	0	28	3.8	2	50	13.6	6	38			
chr18	20083663	C	A	5.7	3	50	4.4	2	43	5.7	2	33	6.9	2	27	13.8	8	50	17.7	11	51			

				Subject 1							Subject 2							Subject 3							
chr18	20083664	A	T	5.7	3	50	2.2	1	44	2.9	1	33	6.9	2	27	10.2	6	53	17.7	11	51				
chr18	21261340	A	G	0.0	0	33	0.0	0	43	2.5	1	39	0.0	0	35	0.0	0	46	21.6	8	29				
chr18	21261344	G	A	28.1	9	23	38.6	17	27	17.5	7	33	34.3	12	23	0.0	0	43	28.9	11	27				
chr18	26089252	A	T	40.9	9	13	59.0	23	16	55.6	20	16	75.6	31	10	93.0	53	4	95.2	40	2				
chr18	28543	A	T	2.9	4	133	4.3	6	132	0.0	0	55	6.6	6	85	4.1	5	117	2.2	2	91				
chr18	34063	C	T	0.0	0	33	0.0	0	52	0.0	0	64	14.8	9	52	4.5	4	85	2.2	2	87				
chr18	39110370	C	A	0.0	0	51	9.8	6	55	0.0	0	35	0.0	0	49	0.0	0	63	0.0	0	46				
chr18	40689656	C	T	0.0	0	48	7.5	4	49	0.0	0	28	0.0	0	44	0.0	0	61	0.0	0	42				
chr18	45023297	A	G	41.0	25	36	33.3	18	36	0	32	0	0	36	0	50.0	25	25	75.0	24	8				
chr18	49767	G	C	2.8	2	69	2.6	2	76	0.0	0	52	10.8	8	66	2.7	2	71	6.8	5	69				
chr18	50768	C	T	1.8	2	109	1.8	2	110	0.0	0	76	6.1	6	93	2.7	4	146	5.9	7	111				
chr18	50847	C	G	2.0	2	98	2.9	3	101	5.0	4	76	4.3	5	111	0.9	1	106	9.8	12	111				
chr18	51661301	A	C	7.7	2	24	2.9	1	34	0.0	0	32	13.8	4	25	0.0	0	35	0.0	0	36				
chr18	51661305	A	C	3.7	1	26	0.0	0	38	0.0	0	33	16.1	5	26	0.0	0	35	0.0	0	36				
chr18	51661309	A	C	3.8	1	25	0.0	0	38	0.0	0	33	12.9	4	27	0.0	0	34	0.0	0	36				
chr18	57918835	T	A	13.3	4	26	30.4	7	16	0.0	0	29	24.0	6	19	2.8	1	35	4.0	1	24				
chr18	5972904	A	T	0.0	0	35	0.0	0	49	13.8	4	25	7.1	2	26	0.0	0	32	22.6	7	24				
chr18	60753946	C	T	2.0	1	48	0.0	0	55	0.0	0	35	12.9	4	27	0.0	0	58	0.0	0	35				
chr18	66245673	C	G	11.1	4	32	21.2	11	41	26.9	7	19	20.6	7	27	0.0	0	41	12.2	5	36				
chr18	68373382	C	T	37.1	13	22	35.7	10	18	0.0	0	28	26.7	8	22	0.0	0	34	0.0	0	25				
chr19	1063335	C	T	1.4	1	69	12.2	5	36	8.3	1	11	0.0	0	26	4.3	1	22	5.9	1	16				
chr19	15620669	T	C	4.3	2	44	0.0	0	40	0.0	0	45	12.5	4	28	1.8	1	55	0.0	0	40				
chr19	16101161	C	T	0.0	0	70	1.3	1	76	16.1	5	26	35.5	11	20	0.0	0	44	0.0	0	36				
chr19	22221248	T	C	4.1	2	47	7.7	4	48	0.0	0	32	8.5	4	43	0.0	0	57	2.6	1	38				
chr19	23844209	A	G	43.3	13	17	33.3	17	34	13.8	4	25	20.0	5	20	23.9	11	35	16.7	7	35				
chr19	31615221	C	A	0.0	0	23	15.6	5	27	0.0	0	36	0.0	0	28	2.3	1	42	0.0	0	26				
chr19	35866399	A	G	0.0	0	56	2.0	1	48	0.0	0	46	0.0	0	46	0.0	0	50	9.1	4	40				
chr19	43730667	G	A	0.0	0	35	15.9	7	37	0.0	0	40	0.0	0	29	0.0	0	43	0.0	0	39				
chr19	43872155	C	T	1.3	1	79	1.3	1	78	9.5	2	19	5.3	2	36	2.5	1	39	17.5	7	33				
chr19	44861272	G	A	3.6	2	53	5.8	3	49	5.1	2	37	2.4	1	41	0.0	0	62	15.6	7	38				
chr19	44861304	C	T	6.6	4	57	3.6	2	54	5.6	2	34	6.1	3	46	0.0	0	71	20.8	10	38				
chr19	44867953	A	G	11.8	6	45	20.5	8	31	0.0	0	42	22.2	6	21	10.4	8	69	11.1	4	32				
chr19	44867975	C	A	12.0	6	44	17.4	8	38	0.0	0	44	29.0	9	22	15.4	12	66	14.6	6	35				
chr19	44870561	C	T	9.1	2	20	8.7	2	21	4.3	1	22	3.1	1	31	0.0	0	46	11.5	3	23				
chr19	44879723	T	C	24.5	13	40	19.4	7	29	0.0	0	28	13.0	6	40	6.4	3	44	14.0	7	43				
chr19	44879760	T	C	25.6	10	29	23.3	7	23	0.0	0	34	17.1	7	34	7.5	4	49	19.4	7	29				
chr19	44919491	A	G	8.2	4	45	12.5	8	56	0.0	0	28	15.4	4	22	5.1	2	37	7.3	3	38				
chr19	44919515	T	C	9.8	5	46	13.2	9	59	0.0	0	27	19.4	6	25	10.2	5	44	10.6	5	42				
chr19	44919525	A	T	6.1	3	46	7.6	5	61	3.6	1	27	9.1	3	30	0.0	0	53	13.0	6	40				
chr19	47520102	A	G	0.0	0	41	9.1	4	40	4.8	1	20	5.6	2	34	9.1	4	40	5.6	2	34				
chr19	48766153	C	T	0.0	0	55	8.9	5	51	2.9	1	34	0.0	0	47	0.0	0	37	0.0	0	46				
chr19	49930970	G	C	30.2	13	30	22.7	5	17	11.1	3	24	22.7	5	17	9.4	3	29	23.1	6	20				
chr19	55129049	G	T	19.0	4	17	34.0	16	31	26.1	6	17	41.4	12	17	35.9	14	25	18.4	7	31				
chr19	56275791	T	C	5.9	5	80	6.5	6	87	0.0	0	49	0.0	0	77	7.0	8	106	5.6	4	67				
chr19	56276217	A	G	35.0	21	39	45.7	32	38	8.6	3	32	23.5	12	39	8.4	7	76	7.5	5	62				
chr20	11311221	C	A	44.4	12	15	32.4	11	23	45.2	14	17	56.7	17	13	25.6	11	32	20.0	7	28				
chr20	12011045	C	G	0.0	0	28	17.1	6	29	0.0	0	34	0.0	0	37	0.0	0	57	0.0	0	56				

				Subject 1							Subject 2							Subject 3						
				T	C	7.1	3	39	25.0	8	24	11.5	3	23	21.2	7	26	11.1	7	56	20.0	7	28	
chr20	13530788	T	C	7.1	3	39	25.0	8	24	11.5	3	23	21.2	7	26	11.1	7	56	20.0	7	28			
chr20	1746819	A	G	28.6	2	5	44.4	4	5	3.4	1	28	35.7	10	18	20.8	5	19	3.1	1	31			
chr20	25735665	A	C	0.0	0	59	12.5	11	77	9.0	9	91	11.5	11	85	10.2	15	132	7.6	8	97			
chr20	25826675	C	G	1.4	2	139	6.3	8	120	13.0	10	67	7.2	8	103	8.5	14	151	7.5	8	98			
chr20	25859201	C	T	15.1	8	45	4.6	3	62	2.6	1	38	10.8	4	33	0.0	0	59	10.4	5	43			
chr20	25873003	T	C	6.1	2	31	5.9	2	32	0.0	0	48	9.3	4	39	3.8	3	75	9.8	5	46			
chr20	25894405	G	A	2.0	1	49	18.3	11	49	13.0	3	20	14.6	6	35	14.3	10	60	7.5	3	37			
chr20	25907144	A	G	2.9	1	33	13.0	7	47	2.3	1	43	11.8	6	45	7.1	5	65	10.5	6	51			
chr20	25980596	G	T	10.0	5	45	9.4	5	48	2.7	1	36	11.1	4	32	0.0	0	53	15.0	6	34			
chr20	26124454	G	T	0.0	0	76	1.4	1	70	0.0	0	86	5.5	4	69	2.8	3	104	1.5	1	67			
chr20	26124460	C	T	0.0	0	76	1.3	1	77	1.1	1	86	5.4	4	70	2.8	3	104	1.4	1	69			
chr20	26135089	T	C	4.3	2	44	14.8	8	46	2.8	1	35	13.5	5	32	9.1	5	50	21.1	8	30			
chr20	26146027	C	T	0.0	0	54	7.1	5	65	3.6	2	53	3.2	2	60	3.8	3	77	7.5	4	49			
chr20	26173334	C	G	2.9	1	34	0.0	0	26	0.0	0	38	0.0	0	27	0.0	0	51	10.0	4	36			
chr20	26200683	T	C	1.4	2	138	3.3	7	203	0.0	0	184	0.0	0	162	0.0	0	264	0.0	0	166			
chr20	26237349	T	A	10.2	5	44	8.7	4	42	0.0	0	36	16.2	6	31	12.3	7	50	5.8	3	49			
chr20	26251366	G	A	2.6	3	112	8.0	9	103	0.0	0	73	5.0	5	96	6.0	8	126	4.3	4	89			
chr20	29429839	C	A	0.0	0	80	0.0	0	94	0.0	0	47	8.2	5	56	0.0	0	98	0.0	0	88			
chr20	29445212	C	T	0.0	0	51	7.4	4	50	8.7	4	42	4.3	2	45	4.1	3	71	9.6	5	47			
chr20	29449318	G	A	0.0	0	60	12.3	8	57	5.6	4	68	5.5	4	69	8.2	8	89	6.3	5	74			
chr20	29453685	G	A	1.3	2	154	0.6	1	156	0.0	0	92	6.9	7	95	4.0	5	120	6.7	8	112			
chr20	29457117	T	C	2.6	2	76	2.4	2	81	1.1	1	94	1.1	1	86	0.0	0	117	4.3	6	134			
chr20	29498078	T	A	9.8	5	46	19.1	13	55	20.5	8	31	23.5	8	26	17.0	9	44	17.0	8	39			
chr20	29499483	T	C	10.8	4	33	5.9	2	32	2.6	1	38	25.0	11	33	2.5	1	39	15.6	5	27			
chr20	29585670	G	T	1.6	1	60	4.5	5	105	0.0	0	65	8.0	6	69	6.8	7	96	2.6	2	76			
chr20	29585690	T	G	0.0	0	85	8.4	10	109	6.5	5	72	5.1	4	74	8.1	9	102	4.8	4	79			
chr20	29594173	G	C	0.0	0	89	7.4	8	100	8.6	12	127	5.0	6	115	5.5	10	172	4.6	7	145			
chr20	29595824	C	A	2.6	4	151	2.0	3	148	0.0	0	121	6.3	7	105	5.8	12	195	8.7	13	136			
chr20	29596273	C	T	6.7	9	125	7.6	9	110	0.0	0	60	6.3	5	75	8.9	7	72	4.1	4	93			
chr20	29612822	C	T	1.2	3	252	3.9	12	295	4.3	10	224	2.5	7	271	2.7	12	436	1.7	6	351			
chr20	29612923	C	T	4.3	7	157	6.5	14	203	1.3	2	150	6.8	10	138	6.3	15	223	4.2	8	184			
chr20	29619907	C	T	6.0	5	78	4.9	4	77	0.9	1	111	7.8	8	95	3.3	7	204	2.8	4	140			
chr20	29623541	A	G	4.8	5	99	2.6	3	114	0.7	1	139	2.3	3	128	0.9	2	216	3.9	8	199			
chr20	29642281	C	A	1.1	1	90	2.9	2	67	4.2	2	46	10.0	6	54	0.0	0	105	5.5	7	121			
chr20	29642323	G	C	3.8	2	50	2.0	1	49	0.0	0	28	7.5	3	37	0.0	0	75	5.0	5	96			
chr20	29998625	A	G	15.6	7	38	23.2	13	43	0.0	0	34	0.0	0	33	8.1	3	34	19.0	8	34			
chr20	447281	G	A	0.0	0	4	20.0	2	8	61.1	11	7	53.3	8	7	0.0	0	33	16.0	4	21			
chr20	52266803	C	T	0.0	0	58	10.0	5	45	6.3	2	30	10.3	3	26	10.4	5	43	9.7	3	28			
chr20	59676836	G	A	1.6	1	60	10.7	6	50	4.8	1	20	10.7	3	25	13.3	6	39	13.8	4	25			
chr20	62315230	G	C	8.1	3	34	13.8	8	50	18.8	6	26	18.2	6	27	0.0	0	30	19.4	6	25			
chr20	62550778	C	T	0.0	0	103	0.0	0	82	4.0	1	24	16.2	6	31	0.0	0	34	0.0	0	31			
chr21	10009734	G	A	0.0	0	120	0.0	0	147	2.1	4	188	1.1	2	181	1.7	4	231	3.6	7	188			
chr21	10012750	T	A	6.2	6	91	13.5	17	109	9.2	11	109	10.0	9	81	8.2	15	169	8.2	9	101			
chr21	10016542	C	A	0.5	1	203	4.7	10	205	0.4	1	255	0.0	0	267	3.9	12	292	4.2	11	250			
chr21	10098881	T	C	0.0	0	201	0.0	0	163	0.5	1	194	5.0	10	192	7.0	19	252	6.3	12	178			
chr21	10129528	C	T	0.0	0	29	0.0	0	29	21.9	7	25	5.6	2	34	3.0	1	32	15.2	7	39			
chr21	10132252	C	T	0.0	0	72	6.6	7	99	2.3	3	129	4.6	7	145	6.3	10	149	8.9	14	144			

				Subject 1						Subject 2						Subject 3					
				C	A	0.0	0	225	0.0	0	226	2.2	4	179	2.8	7	239	1.5	4	257	4.1
chr21	10158959	C	A	0.0	0	225	0.0	0	226	2.2	4	179	2.8	7	239	1.5	4	257	4.1	11	257
chr21	10161232	C	T	2.3	3	127	2.7	4	143	3.7	6	157	1.7	3	171	1.6	3	190	4.6	8	167
chr21	10422164	G	A	3.8	6	151	5.8	8	129	0.0	0	78	2.9	3	101	1.9	3	156	5.3	7	124
chr21	10483568	T	A	4.5	4	85	7.8	9	107	3.8	4	102	6.8	7	96	0.0	0	119	4.5	5	107
chr21	10522438	G	C	47.8	11	12	20.0	6	24	25.0	3	9	10.0	1	9	4.2	1	23	28.6	4	10
chr21	10608414	T	C	7.6	18	219	7.9	17	197	1.8	2	109	5.1	7	129	3.2	5	153	6.8	9	123
chr21	10610420	G	T	0.0	0	180	0.5	1	196	0.0	0	69	6.0	6	94	0.0	0	106	1.0	1	98
chr21	10640870	C	T	0.0	0	60	0.0	0	70	20.0	5	20	18.4	7	31	0.0	0	37	19.1	9	38
chr21	10642141	G	T	2.7	3	110	2.8	3	103	0.0	0	77	7.0	7	93	1.5	2	128	0.0	0	115
chr21	10642161	C	A	3.7	4	103	1.8	2	110	1.1	1	93	8.0	8	92	1.4	2	142	2.3	3	126
chr21	10876240	T	G	9.1	4	40	16.4	10	51	0.0	0	24	24.0	6	19	0.0	0	48	2.6	1	38
chr21	10876246	C	T	9.1	4	40	19.4	12	50	0.0	0	24	23.1	6	20	0.0	0	49	0.0	0	37
chr21	14438730	G	A	0.0	0	31	24.1	7	22	0.0	0	54	0.0	0	36	0.0	0	25	0.0	0	45
chr21	14528394	C	T	8.2	8	90	9.1	10	100	12.2	5	36	4.3	2	44	1.4	1	70	7.4	5	63
chr21	14657244	G	A	4.3	2	45	9.0	6	61	0.0	0	38	2.2	1	44	4.2	2	46	3.8	2	51
chr21	14663537	G	T	0.0	0	39	11.3	6	47	0.0	0	28	0.0	0	40	2.4	1	40	0.0	0	31
chr21	14701390	T	C	1.8	1	55	15.6	10	54	10.3	4	35	10.2	5	44	8.9	4	41	9.1	4	40
chr21	14745186	T	C	18.8	15	65	11.7	9	68	0.0	0	25	22.9	8	27	16.0	4	21	6.5	2	29
chr21	14813483	T	G	7.5	4	49	9.7	6	56	0.0	0	28	14.0	8	49	8.1	5	57	15.6	7	38
chr21	14813487	A	G	7.7	4	48	11.7	7	53	3.6	1	27	14.5	9	53	7.7	5	60	16.7	8	40
chr21	15010848	G	C	0.0	0	59	0.0	0	45	0.0	0	32	8.9	4	41	0.0	0	60	0.0	0	44
chr21	15040759	C	T	0.0	0	39	0.0	0	34	0.0	0	33	13.9	5	31	0.0	0	29	3.2	1	30
chr21	15086488	G	C	4.8	3	59	8.9	5	51	0.0	0	31	12.1	4	29	0.0	0	36	0.0	0	30
chr21	15273070	T	C	0.0	0	18	23.1	6	20	33.3	10	20	51.9	14	13	42.2	19	26	17.2	5	24
chr21	15273073	C	A	0.0	0	18	20.0	5	20	36.7	11	19	46.2	12	14	34.9	15	28	13.8	4	25
chr21	22737558	C	T	22.4	15	52	17.4	8	38	25.0	8	24	35.1	13	24	32.5	13	27	14.7	5	29
chr21	27438226	C	T	0.0	0	43	0.0	0	49	0.0	0	36	0.0	0	43	19.4	12	50	26.4	14	39
chr21	29379480	T	C	26.9	14	38	20.0	14	56	9.8	4	37	25.0	8	24	0.0	0	41	19.6	11	45
chr21	33804322	G	A	0.0	0	46	7.6	5	61	20.0	7	28	10.0	5	45	3.7	1	26	6.3	2	30
chr21	9445857	G	T	0.0	0	196	0.0	0	217	3.0	5	161	3.6	7	189	2.3	5	214	5.1	10	188
chr21	9455102	C	T	1.1	2	186	2.5	6	234	2.1	4	186	1.1	2	188	1.0	2	208	3.8	8	205
chr21	9455205	G	A	0.4	1	226	0.4	1	255	1.1	2	176	3.4	6	172	0.4	1	270	0.5	1	214
chr21	9458897	G	C	1.7	4	225	7.8	15	177	1.2	2	169	6.3	11	164	2.8	8	277	2.9	6	202
chr21	9462105	T	C	0.0	0	38	0.0	0	41	0.0	0	43	7.4	4	50	1.1	1	94	1.3	1	79
chr21	9465303	T	C	0.7	1	143	0.6	1	154	0.9	1	112	4.8	6	119	1.7	2	113	2.1	3	143
chr21	9473950	G	A	30.8	33	74	27.0	27	73	0.0	0	67	14.8	13	75	7.9	12	139	15.6	19	103
chr21	9485333	G	A	1.3	1	78	0.0	0	111	0.0	0	102	6.4	6	88	5.5	9	156	3.3	4	116
chr21	9532033	T	C	1.3	1	76	5.5	5	86	0.0	0	89	9.3	8	78	1.9	3	152	0.0	0	115
chr21	9570102	G	A	6.7	7	97	6.3	7	104	0.0	0	90	8.7	8	84	3.7	5	129	3.2	4	122
chr21	9584296	C	T	22.7	17	58	14.8	16	92	1.1	1	90	10.9	7	57	6.5	10	143	6.9	7	95
chr21	9648521	A	G	16.7	21	105	13.2	19	125	5.0	4	76	13.1	11	73	9.4	6	58	14.1	9	55
chr21	9649616	C	A	1.9	3	156	1.5	3	192	0.9	1	114	5.0	6	115	5.8	8	129	7.2	7	90
chr21	9651441	C	T	0.0	0	88	5.8	6	98	3.1	4	125	3.4	4	114	4.2	6	137	3.4	4	115
chr21	9653331	C	T	5.0	10	191	5.0	9	172	1.1	1	91	1.6	2	120	0.0	0	101	6.0	5	79
chr21	9674695	G	T	1.7	4	228	3.1	8	253	2.8	5	175	3.1	6	185	1.5	4	261	5.4	13	228
chr21	9683310	G	C	5.4	8	141	5.0	6	115	1.4	1	73	3.3	3	88	1.0	1	95	6.6	6	85
chr21	9708485	T	C	0.7	1	143	6.3	8	119	8.5	4	43	13.0	6	40	7.8	4	47	8.3	3	33

				Subject 1						Subject 2						Subject 3					
chr21	9719819	G	A	12.5	17	119	7.9	13	152	0.0	0	133	4.5	6	126	3.2	5	151	5.2	8	145
chr21	9721803	A	G	0.0	0	29	23.7	9	29	18.9	7	30	13.3	4	26	13.0	3	20	22.9	8	27
chr21	9735245	C	T	0.8	1	123	0.0	0	155	3.0	4	128	8.9	15	153	0.0	0	155	0.0	0	155
chr21	9848950	C	G	0.0	0	161	0.5	1	186	1.1	1	86	8.8	8	83	1.3	2	149	3.9	6	146
chr21	9898228	T	C	0.7	1	138	3.3	5	147	5.9	13	209	8.5	21	225	3.9	15	374	2.9	9	299
chr21	9898230	A	C	0.7	1	138	4.0	6	145	6.0	13	205	8.7	22	230	4.1	16	374	3.0	9	292
chr21	9932606	G	C	23.7	9	29	14.3	9	54	5.7	4	66	12.0	10	73	3.1	3	95	1.2	1	82
chr21	9941762	T	A	1.2	3	244	3.9	10	247	3.1	4	127	2.6	4	152	3.5	6	167	2.2	4	174
chr21	9942239	G	A	2.1	4	187	5.4	12	212	5.8	11	180	2.1	4	188	2.9	8	266	0.9	2	213
chr21	9943361	A	C	11.4	13	101	8.8	11	114	0.0	0	86	9.7	9	84	6.5	6	87	11.8	12	90
chr21	9946355	C	A	6.4	3	44	9.8	5	46	2.2	1	45	7.1	4	52	2.2	1	44	10.0	5	45
chr21	9952216	G	C	1.2	1	84	0.0	0	81	0.0	0	99	4.6	4	83	0.0	0	131	1.2	1	82
chr21	9980370	C	A	0.0	0	94	0.0	0	85	1.1	1	90	0.0	0	73	0.0	0	86	8.0	7	80
chr22	16226490	A	G	0.8	1	117	5.5	8	138	2.8	4	139	0.8	1	119	0.8	1	122	1.8	2	108
chr22	16875270	C	T	26.7	12	33	27.7	13	34	0.0	0	25	29.6	8	19	16.7	4	20	45.8	11	13
chr22	16875292	G	A	26.3	10	28	22.5	9	31	0.0	0	22	30.0	6	14	10.5	2	17	40.0	8	12
chr22	16904795	A	C	6.0	5	78	9.8	8	74	0.0	0	45	10.4	5	43	9.2	7	69	8.6	7	74
chr22	16923954	A	T	7.7	3	36	11.1	4	32	11.8	6	45	17.8	8	37	17.9	12	55	25.4	16	47
chr22	16926861	A	G	0.0	0	44	0.0	0	51	0.0	0	34	0.0	0	33	0.0	0	58	8.2	4	45
chr22	16929326	C	T	11.8	6	45	15.9	11	58	0.0	0	31	16.7	6	30	10.2	6	53	8.3	4	44
chr22	16958087	G	A	18.2	4	18	19.0	4	17	19.0	4	17	17.4	4	19	3.4	1	28	24.0	6	19
chr22	16958095	A	G	21.7	5	18	33.3	9	18	20.0	5	20	21.7	5	18	3.0	1	32	27.6	8	21
chr22	17036037	G	T	0.0	0	41	1.8	1	56	7.7	3	36	8.7	2	21	2.0	1	48	16.3	7	36
chr22	17036493	C	G	0.0	0	67	10.7	6	50	0.0	0	22	9.5	4	38	8.3	5	55	8.8	5	52
chr22	17038206	G	A	5.6	3	51	1.8	1	54	5.4	2	35	6.7	3	42	1.7	1	58	16.9	10	49
chr22	17240993	C	T	0.0	0	116	0.0	0	104	0.0	0	41	9.1	6	60	5.3	3	54	15.9	10	53
chr22	17241048	G	A	2.2	2	91	14.3	13	78	13.0	6	40	5.8	3	49	9.7	6	56	5.8	3	49
chr22	17365932	T	C	28.2	11	28	28.1	16	41	3.1	1	31	25.7	9	26	25.0	11	33	24.4	11	34
chr22	17384006	G	A	0.0	0	54	0.0	0	75	6.3	6	90	9.4	8	77	3.7	4	104	12.1	11	80
chr22	17390239	C	T	3.3	1	29	0.0	0	35	35.3	12	22	29.0	9	22	8.1	3	34	30.8	16	36
chr22	17496026	A	G	22.2	10	35	23.8	10	32	0.0	0	32	15.6	5	27	19.4	7	29	11.5	3	23
chr22	17496326	C	A	1.5	1	66	10.0	9	81	4.6	3	62	2.9	2	66	2.5	2	78	8.3	5	55
chr22	17496468	G	T	6.3	10	148	5.2	8	146	0.0	0	80	6.7	7	97	6.3	6	89	6.1	6	92
chr22	17504225	T	C	9.8	4	37	2.2	1	44	5.4	3	53	3.1	2	63	0.0	0	46	15.8	9	48
chr22	20316692	G	C	0.0	0	12	0.0	0	14	0.0	0	27	0.0	0	22	0.0	0	41	18.2	4	18
chr22	22641488	C	A	0.0	0	59	5.6	4	67	5.4	2	35	3.8	2	50	3.5	2	55	5.7	2	33
chr22	22642531	C	A	10.5	4	34	7.5	3	37	12.5	5	35	7.7	3	36	0.0	0	63	16.1	5	26
chr22	23246181	C	T	1.5	1	66	0.0	0	71	0.0	0	44	6.8	4	55	0.0	0	52	0.0	0	40
chr22	23814509	T	C	20.0	7	28	2.8	1	35	4.5	1	21	16.0	4	21	0.0	0	28	12.8	5	34
chr22	23814553	C	A	0.0	0	36	0.0	0	39	4.2	1	23	8.3	2	22	0.0	0	34	15.0	6	34
chr22	23983632	T	G	4.9	3	58	7.5	5	62	0.0	0	33	8.7	4	42	2.2	1	44	0.0	0	34
chr22	25011106	G	T	8.9	5	51	17.0	9	44	14.8	4	23	14.3	5	30	0.0	0	45	16.1	5	26
chr22	25016994	C	T	2.5	2	78	8.0	6	69	0.0	0	28	11.1	4	32	7.0	3	40	10.3	4	35
chr22	25038496	A	G	2.9	1	33	0.0	0	34	0.0	0	24	18.2	8	36	8.2	4	45	3.0	1	32
chr22	26783694	T	G	14.6	7	41	17.3	9	43	0.0	0	21	0.0	0	39	85.0	34	6	88.5	23	3
chr22	27352844	T	C	0.0	0	47	0.0	0	34	0.0	0	43	0.0	0	43	3.7	1	26	15.4	4	22
chr22	34305524	G	T	2.9	1	33	36.0	9	16	14.3	4	24	10.0	2	18	18.9	10	43	20.0	8	32

				Subject 1							Subject 2							Subject 3						
				2.0	1	50	0.0	0	46	6.3	2	30	0.0	0	45	0.0	0	47	11.4	5	39			
chr22	37075189	T	C	2.0	1	50	0.0	0	46	6.3	2	30	0.0	0	45	0.0	0	47	11.4	5	39			
chr22	38776379	T	C	8.3	5	55	7.8	5	59	0.0	0	28	11.1	4	32	6.7	4	56	3.4	2	57			
chr22	39037956	G	A	0.0	0	39	9.6	5	47	0.0	0	38	4.9	2	39	24.6	15	46	22.5	9	31			
chr22	39426361	T	A	0.0	0	28	0.0	0	41	0.0	0	25	20.0	7	28	0.0	0	36	0.0	0	21			
chr22	47039077	C	T	7.3	7	89	2.4	2	82	3.2	1	30	15.0	6	34	4.1	2	47	3.0	1	32			
chr22	49132014	G	A	0.0	0	22	17.9	5	23	0.0	0	16	2.6	1	38	30.4	7	16	23.3	10	33			
chr22	49312391	G	A	32.0	24	51	31.9	29	62	0.0	0	27	0.0	0	41	0.0	0	56	11.9	5	37			
chr22	49395510	T	A	26.3	10	28	36.8	14	24	11.1	4	32	24.2	8	25	10.6	5	42	17.6	6	28			
chrX	106297067	G	T	0.0	0	26	0.0	0	25	4.0	1	24	13.8	4	25	0.0	0	43	0.0	0	33			
chrX	109918904	C	T	14.3	3	18	14.3	2	12	12.1	4	29	6.7	2	28	8.7	4	42	24.1	7	22			
chrX	118636210	T	C	0.0	0	25	0.0	0	42	5.7	2	33	18.4	9	40	0.0	0	49	0.0	0	45			
chrX	125913521	A	G	0.0	0	2	0.0	0	3	39.1	9	14	26.7	8	22	6.5	2	29	20.8	10	38			
chrX	127890836	G	A	33.3	3	6	0.0	0	4	20.0	6	24	40.0	8	12	15.8	3	16	28.6	6	15			
chrX	128428241	A	G	0.0	0	4	0.0	0	9	0.0	0	21	30.8	4	9	14.3	1	6	15.4	2	11			
chrX	135345583	C	T	0.0	0	15	0.0	0	20	9.1	2	20	29.0	9	22	30.0	9	21	54.3	25	21			
chrX	135345587	C	T	0.0	0	15	0.0	0	20	8.3	2	22	25.0	8	24	25.7	9	26	44.4	20	25			
chrX	141472687	A	G	46.7	7	8	47.4	9	10	42.9	12	16	62.9	22	13	50.0	23	23	38.9	14	22			
chrX	145705905	C	A	27.6	8	21	30.0	12	28	8.9	4	41	12.0	6	44	10.7	6	50	12.8	5	34			
chrX	145705907	A	C	29.6	8	19	30.0	12	28	9.1	4	40	11.8	6	45	11.1	6	48	15.8	6	32			
chrX	153366803	G	A	0.0	0	24	0.0	0	28	0.0	0	27	31.4	11	24	34.1	14	27	44.4	12	15			
chrX	171242	G	C	0.0	0	58	0.0	0	85	0.0	0	34	0.0	0	29	0.0	0	58	10.3	4	35			
chrX	38974822	C	G	0.0	0	30	11.8	4	30	0.0	0	27	0.0	0	36	44.4	20	25	47.5	19	21			
chrX	42811826	C	T	36.4	4	7	27.3	3	8	16.1	5	26	13.3	4	26	0.0	0	26	24.2	8	25			
chrX	43408223	G	A	0.0	0	22	0.0	0	19	4.0	1	24	4.8	1	20	0.0	0	27	10.0	3	27			
chrX	5091100	T	C	0.0	0	14	0.0	0	25	7.9	3	35	20.6	7	27	0.0	0	24	22.8	13	44			
chrX	52647729	A	G	3.2	1	30	20.0	5	20	0.0	0	24	13.8	4	25	6.3	3	45	9.3	5	49			
chrX	53908331	T	C	0.0	0	18	22.2	4	14	0.0	0	31	0.0	0	29	12.5	4	28	2.6	1	38			
chrX	58567320	A	T	0.0	0	34	0.0	0	29	0.6	1	153	7.5	9	111	0.0	0	194	0.0	0	164			
chrX	61683511	T	A	1.2	3	239	1.6	5	299	1.1	5	459	2.4	14	576	2.1	16	734	1.6	13	800			
chrX	61692256	G	A	0.0	0	220	0.0	0	178	2.1	2	92	2.6	4	152	0.7	2	271	2.8	7	243			
chrX	61713495	A	T	0.0	0	89	0.0	0	107	1.3	1	79	4.6	4	83	3.0	6	195	0.0	0	142			
chrX	68424573	C	T	24.3	9	28	18.8	6	26	3.3	1	29	3.1	1	31	11.5	3	23	17.9	5	23			
chrX	68424574	T	C	24.3	9	28	21.2	7	26	0.0	0	30	2.9	1	33	0.0	0	26	0.0	0	28			
chrX	79414128	T	A	0.0	0	17	33.3	4	8	3.4	1	28	3.2	1	30	27.8	10	26	28.6	8	20			
chrX	89520495	T	C	0.0	0	12	0.0	0	14	15.2	5	28	15.0	6	34	7.7	3	36	33.3	10	20			

Table S7. Allele frequencies from 1000 Genomes Project exomes.

Allele frequencies and read counts for C and T base calls (G and A bottom strand) from exomes with greater than 100X read depth at the c.548G>A site. DP denotes read depth of C and T base calls at the site in question. %Mutant Allele is (T base calls / C + T base calls) * 100.

Sample	C	T	DP	%Mutant Allele
HG01852	453	0	453	0.00
HG01859	432	0	432	0.00
NA18579	432	1	433	0.23
HG00436	430	0	430	0.00
HG01855	427	0	427	0.00
HG01920	426	0	426	0.00
HG00427	424	0	424	0.00
HG00259	420	0	420	0.00
HG01632	416	0	416	0.00
HG00556	412	0	412	0.00
HG01531	412	0	412	0.00
HG01844	409	0	409	0.00
HG01917	407	0	407	0.00
HG01883	406	1	407	0.25
HG02371	403	0	403	0.00
HG00524	401	0	401	0.00
HG02239	401	0	401	0.00
HG02409	400	1	401	0.25
HG01846	399	0	399	0.00
NA21143	399	0	399	0.00
NA18623	398	0	398	0.00
HG00452	396	0	396	0.00
HG02386	396	0	396	0.00
HG02355	393	1	394	0.25
NA18951	393	0	393	0.00
HG02373	392	0	392	0.00
HG01678	388	0	388	0.00
HG02012	387	0	387	0.00
HG02351	387	0	387	0.00
HG00983	384	1	385	0.26
HG01893	383	1	384	0.26
HG02146	383	0	383	0.00
NA20585	383	0	383	0.00
HG02399	382	0	382	0.00
NA19087	382	0	382	0.00
HG01029	381	0	381	0.00
HG01861	381	0	381	0.00
HG01858	380	1	381	0.26
HG02353	380	0	380	0.00
HG02406	380	1	381	0.26
NA12413	380	0	380	0.00
HG01524	378	0	378	0.00
HG01857	378	0	378	0.00
HG01853	376	0	376	0.00
HG01918	376	0	376	0.00
HG00136	375	0	375	0.00
HG02053	374	0	374	0.00
HG02060	374	0	374	0.00
HG02363	374	1	375	0.27
HG01700	373	0	373	0.00
HG01892	373	0	373	0.00
HG00406	372	0	372	0.00
HG00866	372	0	372	0.00
HG01804	372	0	372	0.00

HG01509	370	0	370	0.00
HG00476	369	0	369	0.00
HG01849	369	1	370	0.27
NA19088	369	0	369	0.00
NA19256	369	0	369	0.00
HG00252	368	0	368	0.00
HG01082	368	0	368	0.00
NA20313	368	0	368	0.00
NA21144	368	0	368	0.00
HG01882	367	0	367	0.00
HG00449	365	1	366	0.27
HG01815	365	0	365	0.00
HG01915	365	0	365	0.00
NA18945	365	0	365	0.00
HG02271	364	1	365	0.27
HG02375	361	0	361	0.00
HG01921	360	0	360	0.00
HG01923	360	0	360	0.00
HG01028	357	1	358	0.28
HG01840	357	0	357	0.00
NA19147	356	1	357	0.28
HG01536	355	1	356	0.28
HG01686	355	0	355	0.00
NA11894	355	0	355	0.00
NA19257	355	0	355	0.00
HG01843	354	1	355	0.28
NA12828	354	1	355	0.28
HG02151	353	0	353	0.00
HG02383	353	0	353	0.00
HG02131	352	2	354	0.56
HG01848	351	2	353	0.57
HG02215	351	0	351	0.00
NA18577	351	0	351	0.00
NA18909	351	0	351	0.00
NA20543	351	0	351	0.00
HG01578	349	0	349	0.00
HG01595	349	0	349	0.00
HG01684	349	0	349	0.00
HG01816	349	2	351	0.57
HG00537	348	1	349	0.29
HG00257	346	1	347	0.29
HG01791	346	1	347	0.29
HG02387	346	0	346	0.00
HG02407	345	0	345	0.00
HG02374	344	0	344	0.00
NA19189	344	1	345	0.29
HG01695	343	0	343	0.00
HG01809	343	0	343	0.00
HG02379	343	0	343	0.00
HG01108	342	0	342	0.00
HG01680	342	0	342	0.00
HG02250	342	0	342	0.00
HG01083	341	0	341	0.00
NA07037	341	0	341	0.00
NA20589	341	0	341	0.00
NA18943	340	0	340	0.00
HG02364	339	0	339	0.00
NA19108	339	0	339	0.00
HG01841	338	0	338	0.00
HG01850	337	0	337	0.00
HG01990	337	0	337	0.00
NA12827	337	1	338	0.30

NA18536	337	0	337	0.00
HG00108	336	0	336	0.00
NA12776	336	1	337	0.30
NA12892	336	0	336	0.00
HG00525	335	0	335	0.00
NA18622	335	0	335	0.00
HG01799	334	1	335	0.30
HG01982	334	0	334	0.00
NA18606	334	0	334	0.00
HG01577	333	1	334	0.30
NA18952	333	0	333	0.00
HG00531	332	0	332	0.00
NA18907	332	0	332	0.00
HG02401	331	0	331	0.00
HG00274	330	0	330	0.00
HG00310	330	0	330	0.00
HG01842	330	0	330	0.00
HG02382	330	0	330	0.00
HG01796	329	0	329	0.00
HG02142	329	1	330	0.30
NA19225	329	0	329	0.00
HG01879	328	2	330	0.61
HG02391	328	0	328	0.00
NA21142	328	0	328	0.00
HG00375	327	0	327	0.00
HG02397	327	0	327	0.00
NA12777	327	0	327	0.00
NA20582	327	0	327	0.00
NA18596	326	0	326	0.00
HG00473	325	0	325	0.00
HG00543	325	0	325	0.00
HG01069	325	0	325	0.00
HG01085	325	0	325	0.00
HG01107	324	1	325	0.31
HG01801	324	0	324	0.00
HG02147	324	0	324	0.00
HG02402	324	0	324	0.00
NA18593	324	0	324	0.00
NA20753	324	0	324	0.00
HG01795	323	0	323	0.00
NA18559	322	1	323	0.31
HG00478	321	1	322	0.31
HG00513	321	0	321	0.00
HG01810	321	0	321	0.00
HG01958	321	0	321	0.00
HG02238	321	0	321	0.00
HG00154	320	1	321	0.31
HG00512	320	2	322	0.62
HG01806	320	0	320	0.00
NA18543	320	0	320	0.00
NA18916	320	0	320	0.00
HG02134	319	0	319	0.00
HG02398	319	0	319	0.00
NA18602	319	1	320	0.31
NA18858	319	0	319	0.00
HG00332	318	0	318	0.00
HG00864	318	0	318	0.00
NA12546	318	0	318	0.00
HG01798	317	0	317	0.00
HG02381	317	0	317	0.00
NA11933	317	0	317	0.00
NA18612	317	0	317	0.00

HG00139	316	0	316	0.00
HG00437	316	0	316	0.00
HG01797	316	0	316	0.00
HG02377	316	0	316	0.00
HG02395	316	0	316	0.00
HG01845	315	0	315	0.00
NA18561	315	1	316	0.32
NA20756	315	0	315	0.00
HG02232	314	0	314	0.00
HG02233	314	0	314	0.00
NA11931	314	1	315	0.32
NA18523	314	0	314	0.00
NA19107	314	1	315	0.32
HG01860	313	2	315	0.63
NA20765	313	1	314	0.32
HG01800	312	1	313	0.32
HG00246	311	0	311	0.00
HG01924	311	0	311	0.00
HG02384	311	0	311	0.00
NA20754	311	0	311	0.00
NA20863	311	0	311	0.00
HG01675	310	0	310	0.00
HG01599	309	0	309	0.00
NA12749	309	0	309	0.00
HG02067	308	1	309	0.32
HG02394	308	0	308	0.00
HG00479	307	0	307	0.00
NA18511	307	0	307	0.00
NA18861	307	0	307	0.00
HG01052	306	1	307	0.33
HG01528	306	0	306	0.00
HG01702	306	0	306	0.00
HG01985	306	0	306	0.00
HG02137	306	0	306	0.00
HG02260	306	1	307	0.33
HG02385	305	0	305	0.00
NA12347	305	0	305	0.00
NA18530	305	1	306	0.33
NA20588	305	0	305	0.00
NA21141	305	0	305	0.00
HG00276	304	0	304	0.00
HG01173	304	0	304	0.00
HG01600	304	0	304	0.00
HG01802	304	0	304	0.00
HG01847	304	0	304	0.00
HG02130	304	0	304	0.00
NA12287	304	0	304	0.00
HG00280	303	1	304	0.33
HG01170	303	0	303	0.00
NA12348	303	0	303	0.00
NA20757	303	0	303	0.00
HG01506	302	0	302	0.00
HG02031	302	0	302	0.00
NA18947	302	0	302	0.00
HG01537	301	0	301	0.00
HG00315	300	0	300	0.00
HG00657	300	0	300	0.00
HG00851	300	0	300	0.00
HG00620	299	0	299	0.00
HG01597	299	1	300	0.33
HG01673	299	1	300	0.33
HG02064	299	2	301	0.66

HG02388	299	0	299	0.00
NA12778	299	0	299	0.00
NA20752	299	0	299	0.00
HG00171	297	0	297	0.00
NA11893	297	0	297	0.00
NA18621	297	0	297	0.00
HG00683	296	0	296	0.00
HG01631	296	0	296	0.00
NA20544	296	0	296	0.00
HG00651	294	1	295	0.34
HG00653	294	0	294	0.00
HG00346	293	0	293	0.00
HG01813	293	0	293	0.00
NA11932	293	0	293	0.00
HG00254	292	0	292	0.00
HG01986	292	1	293	0.34
HG02360	292	1	293	0.34
NA18571	292	0	292	0.00
NA18942	292	0	292	0.00
HG00251	291	0	291	0.00
HG00656	291	0	291	0.00
HG02356	291	0	291	0.00
NA12383	291	0	291	0.00
NA19190	291	0	291	0.00
NA20759	291	0	291	0.00
HG02396	290	0	290	0.00
NA20867	289	0	289	0.00
HG00109	288	0	288	0.00
HG00174	288	0	288	0.00
HG00536	288	0	288	0.00
HG00684	288	0	288	0.00
HG01389	288	0	288	0.00
HG01530	288	0	288	0.00
HG01596	288	0	288	0.00
HG02136	288	1	289	0.35
NA18572	288	0	288	0.00
HG00271	287	1	288	0.35
HG01682	287	0	287	0.00
HG01808	287	0	287	0.00
HG01851	287	0	287	0.00
HG02390	286	0	286	0.00
HG02392	286	0	286	0.00
HG02133	286	3	289	1.04
HG00277	285	0	285	0.00
HG00326	285	0	285	0.00
NA20868	285	0	285	0.00
HG01880	284	0	284	0.00
NA19129	284	0	284	0.00
HG00236	283	0	283	0.00
HG01051	283	0	283	0.00
HG01354	283	0	283	0.00
HG01896	283	2	285	0.70
NA18940	283	0	283	0.00
HG00268	282	0	282	0.00
HG01807	282	0	282	0.00
HG02070	282	1	283	0.35
NA12775	282	0	282	0.00
NA18603	282	0	282	0.00
NA18620	282	0	282	0.00
HG00608	281	0	281	0.00
HG00705	281	0	281	0.00
HG01679	281	1	282	0.35

HG02061	281	0	281	0.00
NA18557	281	1	282	0.35
NA18944	281	0	281	0.00
HG02380	280	0	280	0.00
HG02389	280	1	281	0.36
NA20760	280	0	280	0.00
NA11892	279	0	279	0.00
HG00110	279	3	282	1.06
HG00335	278	0	278	0.00
HG00699	278	0	278	0.00
HG01350	278	0	278	0.00
HG01914	278	1	279	0.36
NA18544	278	0	278	0.00
HG02051	277	0	277	0.00
HG00232	276	0	276	0.00
HG00278	276	0	276	0.00
HG00418	276	0	276	0.00
HG02372	276	0	276	0.00
NA18609	276	0	276	0.00
HG01525	275	0	275	0.00
NA18611	275	1	276	0.36
HG00881	274	0	274	0.00
HG01513	274	0	274	0.00
HG01794	274	0	274	0.00
HG02050	274	1	275	0.36
HG02259	274	0	274	0.00
HG00442	273	0	273	0.00
NA18546	273	0	273	0.00
NA18636	273	1	274	0.36
HG01086	272	0	272	0.00
HG00249	271	0	271	0.00
HG00619	271	1	272	0.37
HG01812	271	0	271	0.00
HG01510	270	0	270	0.00
HG01676	270	1	271	0.37
HG02013	270	1	271	0.37
NA18549	270	0	270	0.00
NA20864	270	0	270	0.00
HG00458	269	0	269	0.00
HG00704	269	0	269	0.00
HG01353	269	0	269	0.00
HG01811	269	1	270	0.37
HG00692	268	0	268	0.00
HG01685	268	0	268	0.00
HG02058	268	1	269	0.37
NA18548	268	0	268	0.00
NA18605	268	0	268	0.00
NA20581	268	0	268	0.00
NA20586	268	0	268	0.00
NA18517	266	0	266	0.00
NA19114	266	1	267	0.37
NA20755	266	0	266	0.00
NA18608	265	0	265	0.00
NA18613	265	0	265	0.00
HG01983	264	1	265	0.38
HG01070	263	0	263	0.00
NA18545	263	1	264	0.38
NA18573	263	0	263	0.00
NA18532	262	0	262	0.00
NA18563	262	1	263	0.38
HG00337	261	0	261	0.00
HG00534	261	0	261	0.00

NA20758	261	0	261	0.00
HG00982	260	0	260	0.00
NA18597	260	0	260	0.00
HG00978	259	0	259	0.00
HG01817	259	0	259	0.00
HG01694	258	0	258	0.00
HG01805	258	1	259	0.39
HG02367	258	0	258	0.00
HG00330	257	1	258	0.39
HG00613	257	0	257	0.00
HG00275	256	0	256	0.00
HG00284	256	0	256	0.00
HG00650	256	1	257	0.39
HG00844	256	1	257	0.39
HG01334	256	1	257	0.39
HG00125	255	0	255	0.00
NA18633	255	0	255	0.00
HG00345	254	0	254	0.00
HG00590	254	0	254	0.00
HG00542	253	0	253	0.00
HG01512	253	0	253	0.00
HG01873	253	0	253	0.00
HG00111	252	0	252	0.00
NA18570	252	0	252	0.00
NA18562	252	3	255	1.18
HG01375	251	0	251	0.00
HG00318	250	1	251	0.40
HG00341	250	0	250	0.00
HG00472	250	0	250	0.00
HG00690	250	0	250	0.00
HG00879	250	1	251	0.40
HG01060	250	1	251	0.40
HG01104	250	0	250	0.00
HG00281	249	0	249	0.00
HG00707	249	0	249	0.00
NA18555	248	0	248	0.00
NA18948	248	0	248	0.00
HG00654	247	1	248	0.40
HG00708	247	0	247	0.00
HG01762	247	0	247	0.00
HG00273	246	0	246	0.00
HG00662	246	0	246	0.00
HG01351	246	0	246	0.00
NA18595	246	0	246	0.00
HG00581	245	0	245	0.00
HG01507	245	0	245	0.00
HG00701	245	3	248	1.21
HG00428	244	0	244	0.00
HG01598	244	0	244	0.00
NA18576	244	0	244	0.00
HG00344	243	0	243	0.00
NA18564	243	0	243	0.00
NA18949	243	0	243	0.00
HG00263	242	1	243	0.41
HG00331	242	0	242	0.00
HG00530	242	0	242	0.00
HG00451	241	0	241	0.00
HG00353	240	0	240	0.00
HG01174	240	0	240	0.00
HG01527	240	0	240	0.00
HG00702	238	1	239	0.42
HG01031	238	0	238	0.00

HG02032	238	0	238	0.00
HG00121	237	0	237	0.00
HG00382	237	0	237	0.00
NA18537	237	1	238	0.42
HG00342	236	0	236	0.00
HG01072	236	0	236	0.00
HG00285	235	1	236	0.42
HG00329	235	0	235	0.00
HG00313	233	1	234	0.43
HG00533	233	1	234	0.43
HG00580	233	0	233	0.00
HG00672	233	0	233	0.00
HG00253	232	0	232	0.00
HG00325	232	1	233	0.43
NA18610	232	0	232	0.00
HG00320	231	0	231	0.00
HG00321	231	1	232	0.43
HG00663	231	0	231	0.00
HG01046	231	1	232	0.43
HG00237	230	0	230	0.00
HG00282	230	0	230	0.00
HG00323	230	1	231	0.43
HG00445	230	1	231	0.43
HG00463	230	0	230	0.00
NA18637	230	0	230	0.00
HG00140	229	0	229	0.00
HG00446	229	0	229	0.00
HG01954	229	0	229	0.00
NA20542	229	0	229	0.00
HG00422	228	0	228	0.00
HG01870	227	0	227	0.00
HG00137	226	0	226	0.00
HG00138	226	0	226	0.00
HG00261	225	0	225	0.00
HG00607	225	0	225	0.00
HG00698	225	0	225	0.00
HG01872	225	0	225	0.00
HG00113	224	0	224	0.00
HG00324	224	0	224	0.00
NA18534	224	0	224	0.00
HG00501	223	0	223	0.00
HG00689	223	1	224	0.45
HG01365	223	0	223	0.00
HG00500	222	0	222	0.00
HG00336	221	2	223	0.90
HG00378	221	0	221	0.00
HG01390	221	0	221	0.00
HG01886	221	0	221	0.00
HG00407	220	0	220	0.00
HG00309	219	0	219	0.00
HG00327	218	0	218	0.00
HG00376	218	0	218	0.00
HG00671	218	0	218	0.00
HG01871	218	1	219	0.46
NA18635	218	0	218	0.00
HG00250	216	0	216	0.00
HG00693	216	0	216	0.00
HG01366	216	0	216	0.00
HG00328	215	0	215	0.00
HG00381	215	0	215	0.00
HG00448	215	0	215	0.00
HG00421	214	1	215	0.47

HG00584	214	0	214	0.00
HG01974	214	0	214	0.00
HG00343	213	0	213	0.00
HG01105	213	0	213	0.00
HG01977	212	0	212	0.00
NA18582	212	0	212	0.00
HG01761	211	0	211	0.00
HG02072	211	0	211	0.00
NA18526	211	0	211	0.00
NA18542	210	0	210	0.00
NA18599	210	0	210	0.00
HG00256	209	0	209	0.00
HG00260	209	2	211	0.95
HG00589	209	0	209	0.00
HG00443	206	0	206	0.00
HG00583	206	0	206	0.00
NA18566	205	0	205	0.00
HG00319	204	0	204	0.00
HG00383	204	0	204	0.00
HG01970	203	0	203	0.00
HG02073	203	0	203	0.00
NA18624	203	0	203	0.00
HG00419	202	0	202	0.00
HG01061	202	0	202	0.00
HG01757	202	0	202	0.00
NA18552	202	1	203	0.49
HG00956	201	0	201	0.00
HG02057	201	0	201	0.00
NA18953	200	0	200	0.00
HG00339	199	0	199	0.00
HG01973	199	0	199	0.00
HG01374	198	0	198	0.00
HG00614	196	0	196	0.00
HG00334	195	0	195	0.00
HG01756	194	0	194	0.00
HG01874	194	0	194	0.00
NA18550	194	0	194	0.00
HG02069	190	0	190	0.00
HG00464	189	0	189	0.00
HG01171	189	0	189	0.00
HG02478	188	0	188	0.00
NA18547	188	1	189	0.53
NA18592	187	0	187	0.00
HG00338	186	0	186	0.00
HG01504	184	0	184	0.00
HG01976	184	0	184	0.00
HG00557	183	0	183	0.00
HG02048	183	0	183	0.00
NA18486	183	0	183	0.00
HG01073	182	0	182	0.00
HG01953	181	0	181	0.00
NA18912	181	0	181	0.00
NA20761	181	0	181	0.00
HG01971	180	0	180	0.00
HG00475	179	0	179	0.00
HG01878	179	0	179	0.00
HG02002	178	0	178	0.00
NA18632	177	0	177	0.00
HG01500	176	0	176	0.00
HG01968	173	0	173	0.00
HG02471	173	0	173	0.00
NA19347	170	0	170	0.00

HG02049	169	0	169	0.00
NA18558	168	1	169	0.59
HG02014	167	0	167	0.00
HG00731	162	1	163	0.61
HG01967	162	0	162	0.00
HG01110	160	0	160	0.00
NA06986	159	0	159	0.00
NA19060	159	0	159	0.00
NA19331	159	1	160	0.63
NA19068	155	0	155	0.00
NA18960	154	1	155	0.65
HG01618	153	0	153	0.00
HG01771	152	0	152	0.00
NA18522	152	1	153	0.65
NA19235	151	0	151	0.00
NA19247	148	0	148	0.00
HG01572	147	1	148	0.68
NA18982	147	0	147	0.00
NA19346	147	0	147	0.00
HG00734	145	0	145	0.00
HG02470	145	0	145	0.00
NA18867	145	0	145	0.00
HG01054	144	0	144	0.00
HG00641	143	0	143	0.00
NA19063	143	1	144	0.69
HG02449	142	0	142	0.00
NA19058	142	1	143	0.70
NA18964	141	0	141	0.00
NA19066	141	0	141	0.00
HG01167	139	0	139	0.00
NA12889	139	0	139	0.00
NA18983	139	0	139	0.00
NA18999	139	1	140	0.71
NA12842	138	0	138	0.00
HG00732	136	0	136	0.00
HG00129	135	0	135	0.00
HG01049	135	0	135	0.00
HG01111	135	0	135	0.00
NA18539	135	0	135	0.00
NA18989	135	0	135	0.00
NA19004	135	0	135	0.00
NA21100	134	2	136	1.47
HG01521	133	0	133	0.00
NA18516	133	0	133	0.00
HG02299	132	0	132	0.00
NA18501	132	0	132	0.00
NA19130	131	0	131	0.00
NA19000	130	0	130	0.00
HG01048	129	1	130	0.77
NA18535	129	0	129	0.00
NA19012	129	0	129	0.00
HG00262	128	0	128	0.00
HG01055	128	0	128	0.00
NA19065	128	0	128	0.00
NA19172	128	0	128	0.00
NA18853	127	0	127	0.00
HG00457	126	1	127	0.79
HG01094	126	0	126	0.00
NA19102	126	0	126	0.00
NA20818	126	0	126	0.00
NA21099	126	0	126	0.00
NA19007	125	0	125	0.00

NA19334	125	0	125	0.00
HG00308	123	0	123	0.00
NA18910	123	0	123	0.00
NA18959	123	0	123	0.00
NA18870	122	0	122	0.00
NA19474	122	0	122	0.00
NA11918	121	0	121	0.00
HG01198	120	0	120	0.00
NA18873	120	0	120	0.00
HG00737	119	0	119	0.00
NA20344	119	0	119	0.00
HG01101	118	0	118	0.00
HG01183	118	1	119	0.84
HG01197	118	0	118	0.00
HG01204	117	0	117	0.00
HG02489	117	1	118	0.85
HG00188	116	0	116	0.00
HG01191	116	0	116	0.00
NA20815	116	0	116	0.00
NA19116	114	0	114	0.00
NA20341	112	0	112	0.00
HG01182	111	0	111	0.00
HG01746	111	0	111	0.00
NA20336	111	0	111	0.00
NA12890	110	1	111	0.90
NA19070	110	0	110	0.00
NA20828	110	0	110	0.00
NA21090	110	0	110	0.00
NA19439	109	0	109	0.00
HG01168	107	0	107	0.00
NA18538	107	0	107	0.00
NA19093	107	0	107	0.00
NA18868	106	0	106	0.00
NA18984	106	0	106	0.00
NA19003	106	0	106	0.00
HG00155	105	0	105	0.00
HG00739	105	0	105	0.00
NA12400	105	0	105	0.00
NA18499	105	0	105	0.00
NA18533	105	0	105	0.00
NA21102	105	0	105	0.00
NA19900	104	0	104	0.00
NA19648	102	1	103	0.97
HG00245	101	0	101	0.00
NA18961	101	0	101	0.00
NA19056	101	0	101	0.00
NA19213	101	0	101	0.00
NA20910	101	0	101	0.00
NA21097	101	0	101	0.00
HG00185	100	0	100	0.00
HG00242	100	0	100	0.00
HG01066	100	0	100	0.00
HG01519	100	0	100	0.00
HG01864	100	0	100	0.00
HG02292	100	0	100	0.00
NA18908	100	0	100	0.00
NA19471	100	0	100	0.00

File S1. Barcode file for de-multiplexing reads

Filename “barcodes.txt”, delimited by TAB character, line terminator “newline” character.
Barcodes used as input for “splitSam.sh” (File S3), referenced in File S2.

P1_1	TTATAAC
P1_2	TTAATTG
P1_3	AAGTTTT
P1_4	TATTATG
P1_5	ATTAGTT
P1_6	ATTTTAG
P1_7	TATATGT
P1_8	CTATAGT
P1_9	AAATCCT
P1_10	TCAACTA
P1_11	TCATGAT
P1_12	CTAACATCA
P1_13	AAACTTC
P1_14	GGATTTT
P1_15	ATCAACT
P1_16	TACCATA
P1_17	TACACAT
P1_18	ATCCTAA
P1_19	TTGCAAT
P1_20	TTGGTTA
P1_21	CATTACA
P1_22	ACTAATC
P1_23	GTTGATT
P1_24	ACTTCAA
P1_25	TGTTGTA
P1_26	CATATAC
P1_27	TGTGTAT
P1_28	GTTTGTA
P1_29	CCACAAT
P1_30	TTAGCCA
P1_31	GAATCTC
P1_32	AGACCTT
P1_33	TTACGGT
P1_34	AGATTCC
P1_35	GAACTCT
P1_36	CCAGTTA
P1_37	TGCTACA
P1_38	GTCAATC
P1_39	ACCGATT
P1_40	GTCTCAA
P1_41	CACTGTA
P1_42	TGCATAC
P1_43	CACGTAT
P1_44	ACCTTGA
P1_45	TCGTAGT
P1_46	CTGACTA
P1_47	CTGTGAT
P1_48	TCGATCA
P1_49	ATTGACC
P1_50	GCTAACT
P1_51	CGTCATA
P1_52	TATGCAC
P1_53	CGTACAT
P1_54	ATTCCGA
P1_55	TATCGCA
P1_56	GCTCTAA
P1_57	TCACAGC
P1_58	CTAGCTG
P1_59	CTACGAC
P1_60	TCAGTCG
P1_61	CGCTATG
P1_62	ATCTCGG
P1_63	TACTGCG
P1_64	ATCGGTC
P1_65	GCCAGTT
P1_66	GCCTTAG

P1_67	TACGTGC
P1_68	CGCATGT
P1_69	CCGTAAC
P1_70	TTGACCG
P1_71	AGGTCTC
P1_72	GAGCCTT
P1_73	TTGTGGC
P1_74	GAGTTCC
P1_75	AGGCTCT
P1_76	CCGATTG
P1_77	TGTCAAG
P1_78	GTTCCAG
P1_79	TGTACGC
P1_80	CATGCGT
P1_81	GTTAGCC
P1_82	ACTGGCT
P1_83	CATCGTG
P1_84	ACTCTGG
P1_85	CCAACCG
P1_86	CCATGGC
P1_87	CACCAAG
P1_88	ACCCCAAG
P1_89	CACACGC
P1_90	TGCGCGT
P1_91	ACCAGCC
P1_92	GTCGGCT
P1_93	TGCCGTG
P1_94	GTCCTGG
P1_95	CTGCAGC
P1_96	AAGCCCC

File S2. Bpipe⁶ stage definitions and pipeline for aligning and de-multiplexing paired-end Illumina reads.

Filename “align_demultiplex.bpipe” used as input for “bpipe run” command in Bpipe software suite. Stage definitions utilize BWA⁴ for alignments, producing Sequence Alignment/Map⁵ (SAM) formatted output. References File S1 (barcodes.txt) and File S3 (splitSam.sh).

```
@Transform("sam")
bwa_aln_bc_illumina = {
    r1 = async "bwa aln -q $quality -t $threads -B $length $reference ${input1} > ${input1}.sai"
    r2 = async "bwa aln -q $quality -t $threads $reference ${input2} > ${input2}.sai"
    r1.waitFor()
    r2.waitFor()
    exec "bwa sampe $reference ${input1}.sai ${input2}.sai ${input1} ${input2} > $output"
}

split.sam_bc = {
    exec "splitSam.sh $input $barcodes"
}

Bpipe.run {
    bwa_aln_bc_illumina.using(quality:30, threads:4, length:7, reference:"~/reference/hg19.fa") +
    split.sam_bc.using(barcodes:"barcodes.txt")
}
```

File S3. Shell script for splitting BWA aligned SAM files by barcode.

Filename “splitSam.sh” used as an executable shell script in File S2. This script will run on a POSIX compliant operating system using the Bourne Again Shell (Bash) interpreter.

```
#!/bin/sh
if [ $# -eq 0 ] ; then
    echo 'Usage: splitSam.sh input.sam barcodes.txt'
    echo ''
    echo 'barcodes.txt must be two columns with tab delimiter'
    echo 'column1 = barcode name, column2 = barcode sequence'
fi
SAM=$1
BC_FILE=$2

#Capture the SAM header
SAM_H=`samtools view -SH $SAM` 

#Read barcode table into array line by line
#then grep barcoded SAM reads to file
while IFS=$'\t' read -r -a array
do
    sampleName=${array[0]} #barcode name
    BC=${array[1]} #barcode sequence
    BC=${BC%"${BC##*[![:space:]]}"} #remove trailing whitespace
    if grep -q -m 1 -e "BC:Z:$BC" $SAM; then
        printf "$SAM_H\n" > ${sampleName}.sam #write SAM header to file
        grep -e "BC:Z:$BC" $SAM >> ${sampleName}.sam #write barcoded reads
    fi
    printf "BC:Z:$BC\n" >> /tmp/bc #patterns for unmatched reads
done < $BC_FILE

#Write unmatched reads to file
if grep -qv -e "^@" $SAM | grep -qv -f /tmp/bc; then
    grep -v -f /tmp/bc $SAM > unmatched.sam #write unmatched reads
fi
rm /tmp/bc
```

File S4. Bpipe stage definitions and pipeline for counting alleles from de-multiplexed SAM files.

Filename “count_alleles.bpipe” used as input for “bpipe run” command in Bpipe software suite.

```
@Transform("bam")
sam_to_bam = {
    exec "samtools view -bS $input > $output"
}

@Filter("sort")
sort_bam = {
    exec "samtools sort -o -m 4000000000 $input piece > $output"
}

bam_index = {
    exec "samtools index $input"
}

@Transform("mpileup")
count_alleles = {
    exec($/samtools mpileup -d 500000 -A -r $position -B -Q 30 $input > $output/$)
    exec($/echo '' >> $output/$)
    exec($/printf 'C\t' >> $output/$)
    exec($/cut -f5 $output | grep -i -o -e '[c]' | wc -l | tr '\n' '\t' >> $output/$)
    exec($/printf 'T\t' >> $output/$)
    exec($/cut -f5 $output | grep -i -o -e '[t]' | wc -l | tr '\n' '\t' >> $output/$)
    exec($/printf 'A\t' >> $output/$)
    exec($/cut -f5 $output | grep -i -o -e '[a]' | wc -l | tr '\n' '\t' >> $output/$)
    exec($/printf 'G\t' >> $output/$)
    exec($/cut -f5 $output | grep -i -o -e '[g]' | wc -l | tr '\n' '\t' >> $output/$)
    exec($/printf 'DP\t' >> $output/$)
    exec($/cut -f5 $output | grep -i -o -P '[(w)]' | wc -l | tr '\n' '\t' >> $output/$)
}

Bpipe.run {
    "%sam" * [sam_to_bam + sort_bam + bam_index + count_alleles.using(position:"9:80412493-80412493")]
}
```

File S5. Shell script for counting number of alleles from each mapped and de-multiplexed SAM file.

Filename “count_from_pileup.sh”, accepts a single SAM file as input, and prints the number of A,C,T, and G alleles. This script will run on a POSIX compliant operating system using the Bourne Again Shell (Bash) interpreter.

```
#!/bin/sh
for i in $*
do
    printf "$i\t" | tr -d ".sort.mpileup" | sed 's/P1_//'
    tail -n1 $i
    printf "\n"
done | sort -nk1,1
```

References

1. Saunders CT, Wong WSW, Swamy S, Becq J, Murray LJ, Cheetham RK. Strelka: accurate somatic small-variant calling from sequenced tumor-normal sample pairs. *Bioinformatics* 2012;28(14):1811-7.
2. Yandell M, Huff C, Hu H, et al. A probabilistic disease-gene finder for personal genomes. *Genome Research* 2011;21(9):1529-42.
3. Bystrykh LV. Generalized DNA Barcode Design Based on Hamming Codes. *PLoS ONE* 2012;7(5):e36852.
4. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics* 2009;25(14):1754-60.
5. Li H, Handsaker B, Wysoker A, et al. The Sequence Alignment/Map format and SAMtools. *Bioinformatics* 2009;25(16):2078-9.
6. Sadedin SP, Pope B, Oshlack A. Bpipe: a tool for running and managing bioinformatics pipelines. *Bioinformatics* 2012;28(11):1525-6.